mRNA was detected in samples from liver, kidney, pancreas, stomach, thyroid, prostate and with multiple human tissues blots (CLONTECH) using a full-length human hepsin cDNA. Hepsin Fig. 1. Northern analysis of hepsin mRNA in human tissues. Northern hybridization was performed



heart brain placenta lung liver skeletal muscle kidney pancreas stomach thyroid spinal cord lymph node trachea adrenal gland bone marrow spleen thymus prostate testis ovary small intestine colon peripheral blood leukocyte

Relative Level of Hepsin mRNA Expression

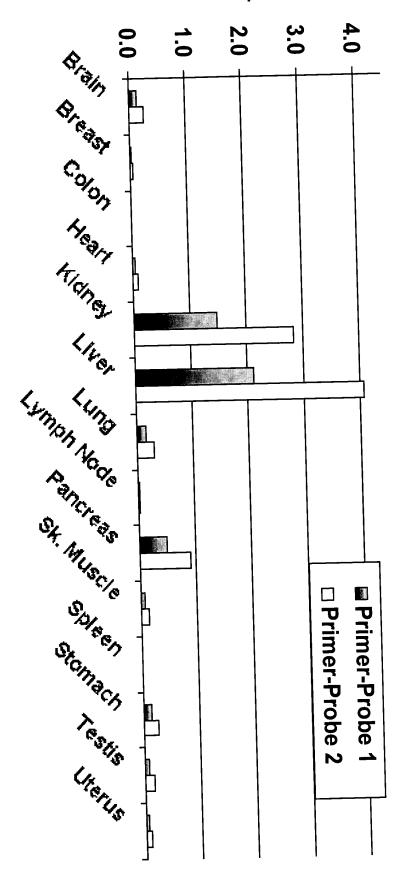


Fig. 2. Taqman analysis of hepsin mRNA expression in human tissues. Taqman-based quantitative PCR analysis of hepsin mRNA expression was performed using two sets of hepsin-specific primers and kidney. (Primer-Probes 1 and 2). High levels of hepsin mRNA expression were detected in samples from liver

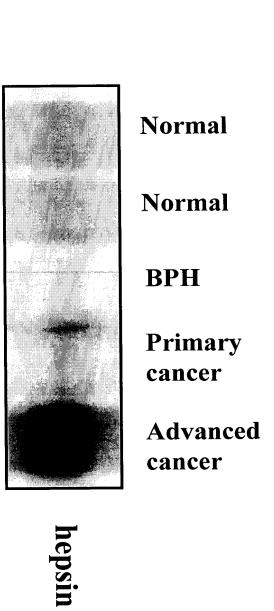
and prostate cancer tissues. Northern blot was prepared and hybridized with a human hepsin cDNA ratio of hepsin/GAPDH mRNA was \sim 6-fold higher in the advanced cancer than in normal prostate, probe. Hepsin mRNA expressed was significantly higher in an advanced prostate cancer sample. The Fig. 3. Hepsin mRNA expression in prostate cancer. mRNA was isolated from normal prostate, BPH **BPH** or primary prostate cancer. Prostate Rormal Prostate Grado 3 Grado 4

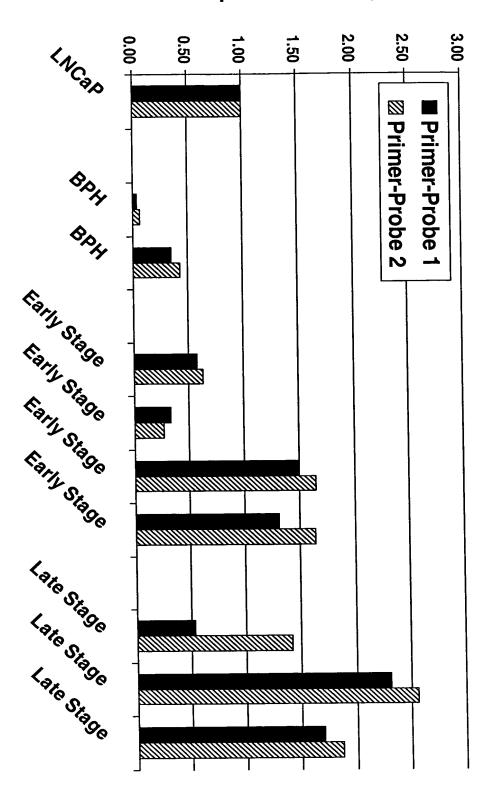
Hepsin/GAPDH

(fold increase)

თ თ

ယ



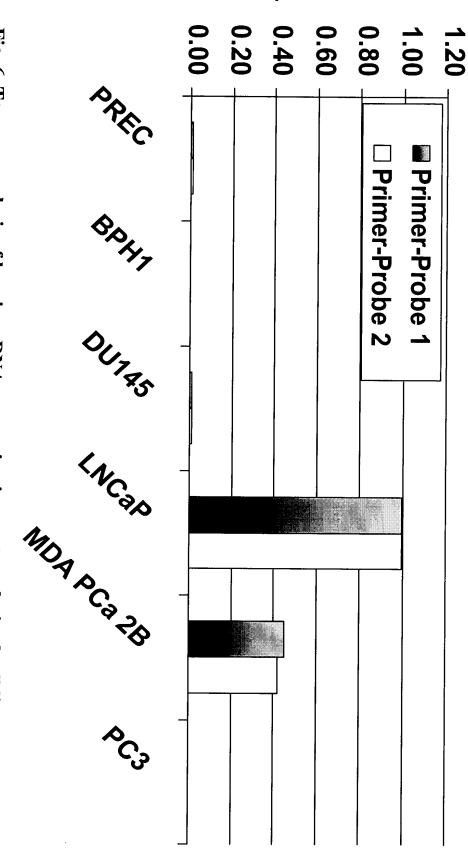


performed using two set of primers specific for human hepsin (Primer-Probes 1 and 2). Modest to more dramatic Figure 4. Taqman analysis of hepsin mRNA expression in prostate tissue. mRNA samples were prepared from LNCaP cells, BPH and prostate cancer (Gleason grade 3 and 4) tissues. Quantitative increases of hepsin mRNA expression were detected in prostate cancer samples. PCR analysis was

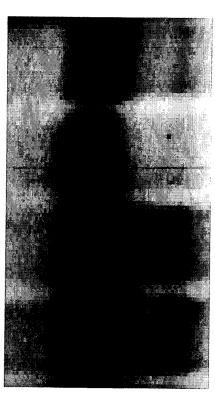
Fig. 5. Northern analysis of hepsin mRNA expression in prostate-derived cell lines. mRNA was with ethdium bromide to show equal sample loading. isolated from prostate-derived cell lines, LNCaP, PC3, MDA PCa2b, BPH-1, DU145, PZ HPV7, in LNCaP, MDA Pca 2b and HepG2 cells (upper panel). As a control, the agarose gel was stained CA HPV10 and a control cell line, HepG2. Northern analysis detected hepsin mRNA expression

W HepG2 LNCaP PC3 MDA PCa 2b **BPH-1 DU145** PZ HPV7 CA HPV10

Relative Expression of Hepsin mRNA



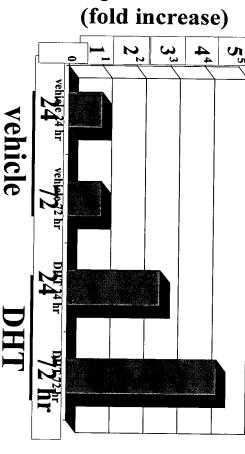
isolated from prostate-derived cell lines. Taqman analysis was performed using two sets of LNCaP and MDA Pca 2B cells. hepsin specific primers (Primer-Probes 1 and 2). Hepsin mRNA expression was detected in Fig. 6. Taqman analysis of hepsin mRNA expression in prostate-derived cell lines. mRNA was



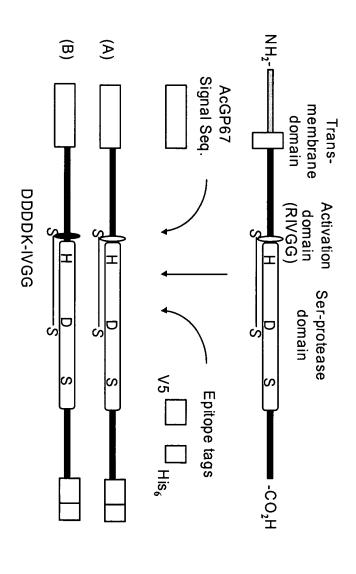
Hepsin

Hepsin/GAPDH 55

B.



re-probed with a GAPDH cDNA. Hepsin mRNA expression was significantly enhanced in samples were isolated. Northern blots were hybridized with a human hepsin cDNA probe and Fig. 7. Up-regulation of hepsin mRNA expression in LNCaP cells by dihydrotestosterone (DHT). LNCaP cells treated with DHT for 24 and 72 hours. LNCaP cells were treated with DHT (10 nM) and harvested at indicted time points. Total RNA



sequence for Arg 162. The mutation will allow hepsin to be activated by enterokinase. sequence coding for an enterokinase recognition peptide, DDDDK, is inserted to replace the coding 5' end and a sequence coding for a V5 epitope and a His6 tag at the 3' end. In construct B, a of hepsin is cloned into vector pAcGP67 that contains a sequence coding for a signal peptide at the hepsin protein is shown on top. To express soluble wild-type hepsin (A), the extracellular domain Fig. 8. Expression of soluble wild-type and mutant hepsins. A schematic presentation of human

FIG9 (1-7) pIRESpuro2W/hepEK_k

1	GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	CAGTACAATC
					GTCATGTTAG
51	TGCTCTGATG	CCGCATAGTT	' AAGCCAGTAT	CTGCTCCCTG	CTTGTGTGTT
					GAACACACAA
101	GGAGGTCGCT	GAGTAGTGCG	CGAGCAAAAT	TTAAGCTACA	ACAAGGCAAG
			GCTCGTTTTA		
151	GCTTGACCGA	CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTGCG
			TTCTTAGACG		
201	CTGCTTCGCG	ATGTACGGGC	CAGATATACG	CGTTGACATT	GATTATTGAC
	GACGAAGCGC	TACATGCCCG	GTCTATATGC	GCAACTGTAA	CTAATAACTG
251	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC	ATTAGTTCAT	AGCCCATATA
	ATCAATAATT	ATCATTAGTT	AATGCCCCAG	TAATCAAGTA	TCGGGTATAT
301	TGGAGTTCCG	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG
	ACCTCAAGGC	GCAATGTATT	GAATGCCATT	TACCGGGCGG	ACCGACTGGC
351	CCCAACGACC	CCCGCCCATT	GACGTCAATA	ATGACGTATG	TTCCCATAGT
	GGGTTGCTGG	GGGCGGGTAA	CTGCAGTTAT	TACTGCATAC	AAGGGTATCA
401	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	ATGGGTGGAC	TATTTACGGT
	TTGCGGTTAT	CCCTGAAAGG	TAACTGCAGT	TACCCACCTG	ATAAATGCCA
451	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC	AAGTACGCCC
	TTTGACGGGT	GAACCGTCAT	GTAGTTCACA	TAGTATACGG	TTCATGCGGG
501	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA
			ATTTACCGGG		
551	CATGACCTTA	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA
			GATGAACCGT		
601	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC	AGTACATCAA	TGGGCGTGGA
	AGCGATAATG	GTACCACTAC	GCCAAAACCG	TCATGTAGTT	ACCCGCACCT
651	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA
			TAAAGGTTCA		
701	TGGGAGTTTG	${\tt TTTTGGCACC}$	AAAATCAACG	GGACTTTCCA	AAATGTCGTA
	ACCCTCAAAC	AAAACCGTGG	TTTTAGTTGC	CCTGAAAGGT	TTTACAGCAT
751	ACAACTCCGC	${\tt CCCATTGACG}$	CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG
			GTTTACCCGC		
801	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA	CTGCTTACTG
			GACCGATTGA		
851	GCTTATCGAA	ATTAATACGA	CTCACTATAG	GGAGACCCAA	GCTTGGTACC
	CGAATAGCTT	TAATTATGCT	GAGTGATATC	CCTCTGGGTT	CGAACCATGG
+3				TDTL	LLW
901	GAGCTCGGAT	CGATATCGCC	ACCATGGAGA	CAGACACACT	CCTGCTATGG
			TGGTACCTCT	GTCTGTGTGA	GGACGATACC
+3		L W V P			P D R S
951	GTACTGCTGC	TCTGGGTTCC	AGGTTCCACT	GGTGACGCTC	CGGACAGGAG
•			TCCAAGGTGA	CCACTGCGAG	GCCTGTCCTC
+3	SD Q E		<u>PVQV</u>	S S A	DARL
1001	TGACCAGGAG	CCGCTGTACC	CAGTGCAGGT	CAGCTCTGCG	GACGCTCGGC
	ACTGGTCCTC	GGCGACATGG	GTCACGTCCA	GTCGAGACGC	CTGCGAGCCG

+3	LM V F D K T E G T W R L L C S S	
1051	THE TRACTOR TO A CALCA GAAGGGACGT GGCGGCTGCT GTGCTCCTCG	
1031	AGTACCAGAA ACTGTTCTGC CTTCCCTGCA CCGCCGACGA CACGAGGAGGA	
+3	B S N A R V A G L S C E E M G T L	
1101	CGCTCTAACG CCAGGGTAGC CGGACTCAGC TGCGAGGAGA TGGGCTTCCT	
	GCGAGATTGC GGTCCCATCG GCCTGAGTCG ACGCTCCTCT ACCCGAAGGA	
+3	IRALTHSELD VIII	
1151	CAGGGCACTG ACCCACTCCG AGCTGGACGT GCGAACGGCG GGCGCCAATG GTCCCGTGAC TGGGTGAGGC TCGACCTGCA CGCTTGCCGC CCGCGGTTAC	
_	GTCCCGTGAC TGGGTGAGGC TCGACCTGCT GGGTGAGGC TCGACCTG	
+3	TO SUPPOSE CHIEFTOTET GTGGACGAGG GGAGGCTGCC CCACACCCAG	
1201	CCTCCACCC GAAGAAGACA CACCTGCTCC CCTCCGACGG GGIGIGGGIC	
+3	RII EVISVCD CPH G N 1 2	ı
1251	AGGCTGCTGG AGGTCATCTC CGTGTGTGAT TGCCCCAGAG GCCGTTTCTT	
1231	TCCGACGACC TCCAGTAGAG GCACACACTA ACGGGGTCTC CGGCAARSIN	•
+3	LAALCQDCGHHRL	,
1301	GGCCGCCATC TGCCAAGACT GTGGCCGCAG GAAGCTGCCC GTGGACGACGCCCCGCGGTAG ACGGTTCTGA CACCGGCGTC CTTCGACGG CACCTGCTGC	:
		_
+3	ACGACAAGAT CGTGGGAGGC CGGGACACCA GCTTGGGCCG GTGGCCGCACC	3
1351	ACGACAAGAT CGTGGGAAGC COOTHETT CGAACCCGGC CACCGGCACC	2
+3	OVSLRYDGAHLUGGG	¬
1401	CARGACCO TTCGCTATGA TGGAGCACAC CTCTGTGGGG GATCCCTGC	r v
	GTTCAGTCGG AAGCGATACT ACCTCGTGTG GAGACACCCC CTAGGGACAC	4.1
+3	S G D W V L I A A H C I	C
1451	CTCCGGGGAC TGGGTGCTGA CAGCCGCCCA CTGCTTCCCG GAGCGGAAC GAGGCCCTG ACCCACGACT GTCGGCGGGT GACGAAGGGC CTCGCCTTG	G
		;
+3	TRETTERE COCATGCCGA GTGTTTGCCG GTGCCGTGGC CCAGGCCTC	T.
1501	CCCAGGACAG GGCTACCGCT CACAAACGGC CACGGCACCG GGTCCGGAC	11.1
+	2 PHGLQLGVQAVVIRUS	<u>.</u>
155	1 CCCCACGGTC TGCAGCTGGG GGTGCAGGCT GTGGTCTACC ACGGGGGCT	.'A.
	GGGGTGCCAG ACGTCGACCC CCACGTCCGA CACCAGATGG TGCCCCGA	.r
+	2 VI P F R D P N S L L	c c
160	1 TCTTCCCTTT CGGGACCCCA ACAGCGAGGA GAACAGCAAC GATATTGCC AGAAGGGAAA GCCCTGGGGT TGTCGCTCCT CTTGTCGTTG CTATAACGC	ЗG
	, eepiPLTEY'U'_	<u>v_</u>
	THE CONTROL OF CONCENCE CTGCCCCTCA CAGAATACAT CCAGCCTG	TG
165	ACCAGGTGGA GAGGTCAGGG GACGGGGAGT GTCTTATGTA GGTCGGAC	210
	2 CIPAAGQALV DG KI	<u>, </u>
170	TRECOMERCIA CTECCECCA GECCTGGTG GATGGCAAGA TCTGTACC	:CD
	ACGGAGGGTC GACGGCCGGT CCGGGACCAC CTACCGTTCT AGACATOG	
	13 ·V T G W G N I U I L	
175	GACGGGCTGG GGCAACACGC AGTACTATGG CCAACAGGCC GGGGTACT CTGCCCGACC CCGTTGTGCG TCATGATACC GGTTGTCCGG CCCCATGA	\GG
	C.I.G.C.C.GALLA.1003 TOTAL	

+3	·QEARVPIISND V CN GAI)
1801	AGGAGGCTCG AGTCCCCATA ATCAGCAATG ATGTCTGCAA TGGCGCTG.	
1801	TCCTCCGAGC TCAGGGGTAT TAGTCGTTAC TACAGACGTT ACCGCGAC	
+3	F Y G N Q I K P K M F C A G Y P	
1851	TTCTATGGAA ACCAGATCAA GCCCAAGATG TTCTGTGCTG GCTACCCC	GA
1031	AAGATACCTT TGGTCTAGTT CGGGTTCTAC AAGACACGAC CGATGGGG	
+3		_E
1901	GGGTGGCATT GATGCCTGCC AGGGCGACAG CGGTGGTCCC TTTGTGTG	TG
	CCCACCGTAA CTACGGACGG TCCCGCTGTC GCCACCAGGG AAACACAC	
+3	EDSISRTPRWRLCGIV	S
1951	AGGACAGCAT CTCTCGGACG CCACGTTGGC GGCTGTGTGG CATTGTGA	
	TCCTGTCGTA GAGAGCCTGC GGTGCAACCG CCGACACACC GTAACACT	
+3	WGTGCALAQKPGVYTK	V ·
2001	TGGGGCACTG GCTGTGCCCT GGCCCAGAAG CCAGGCGTCT ACACCAAA	
	ACCCCGTGAC CGACACGGGA CCGGGTCTTC GGTCCGCAGA TGTGGTTT	
+3	V 3 D 1 II C W	Α.
2051	CAGTGACTTC CGGGAGTGGA TCTTCCAGGC CATAAAGACT CACTCCGA	
	GTCACTGAAG GCCCTCACCT AGAAGGTCCG GTATTTCTGA GTGAGGCT	P.
+3	A 3 d liii V 1 d 2 L 2	
2101	CCAGCGGCAT GGTGACCCAG CTCGAATTCG GTAAGCCTAT CCCTAACC	
_	GGTCGCCGTA CCACTGGGTC GAGCTTAAGC CATTCGGATA GGGATTGG	JGA
+3		nmc
2151	CTCCTCGGTC TCGATTCTAC GCGTACCGGT CATCATCACC ATCACCAT GAGGAGCCAG AGCTAAGATG CGCATGGCCA GTAGTAGTGG TAGTGGTA	
2201	AGTTTAAAGC GGCCGCATAG ATAACTGATC CAGTGTGCTG GAATTAAT TCAAATTTCG CCGGCGTATC TATTGACTAG GTCACACGAC CTTAATTA	
0051	GCTGTCTGCG AGGGCCAGCT GTTGGGGTGA GTACTCCCTC TCAAAAGG	
2251	CGACAGACGC TCCCGGTCGA CAACCCCACT CATGAGGGAG AGTTTTCC	
2301	GCATGACTTC TGCGCTAAGA TTGTCAGTTT CCAAAAACGA GGAGGAT	
2301	CGTACTGAAG ACGCGATTCT AACAGTCAAA GGTTTTTGCT CCTCCTA	
2351	TO THE STATE OF TH	
2331	TATAAGTGGA CCGGGCGCCA CTACGGAAAC TCCCACCGGC GCAGGTA	
2401		
2101	CAGTCTTTC TGTTAGAAAA ACAACAGTTC GAACTCCACA CCGTCCG	
2451	AGATCTGGCC ATACACTTGA GTGACAATGA CATCCACTTT GCCTTTC	тст
	TCTAGACCGG TATGTGAACT CACTGTTACT GTAGGTGAAA CGGAAAG	AGA
2501		
	GGTGTCCACA GGTGAGGGTC CAGGTTGACG TCCAGCTCGT ACGTAGA	TCC
2551		
	CGCCGGTTAA GGCGGGGAGA GGGAGGGGGG GGGGATTGCA ATGACCG	
2601		
	TCGGCGAACC TTATTCCGGC CACACGCAAA CAGATATACA CTAAAAG	
2651		
	GTATAACGGC AGAAAACCGT TACACTCCCG GGCCTTTGGA CCGGGAC	
2701		
	AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT TCCTTAC	G'I"I

FIGURE 9-3

2751			GGAAGCAGTT CCTTCGTCAA		
2801			CCCTTTGCAG GGGAAACGTC		
2851			CAAAAGCCAC GTTTTCGGTG		
2901	TTCCGCCGTG	TTGGGGTCAC	CCACGTTGTG GGTGCAACAC	TCAACCTATC	AACACCTTTC
2951			GCGTATTCAA CGCATAAGTT		
3001	TCTTCCATGG	GGTAACATAC	GGATCTGATC CCTAGACTAG	ACCCCGGAGC	CACGTGTACG
3051	AAATGTACAC	AAATCAGCTC	GTTAAAAAAA CAATTTTTTT	GCAGATCCGG	GGGGCTTGGT
3101	GCCCTGCAC	CAAAAGGAAA	GAAAAACACG CTTTTTGTGC	TACTATTCGA	ACGGTGTTGG
3151	GTGTTCCTCT	GCTGGAAGGT	TGACCGAGTA ACTGGCTCAT	GTTCGGGTGC	CACGCGGAGC
3201	GGTGGGCGCT	GCTGCAGGGG	CGGGCCGTAC GCCCGGCATG	CGTGGGAGCG	GCGGCGCAAG
3251	CGGCTGATGG	GGCGGTGCGC	GGTGTGGCAG	CTGGGCCTGG	
3301	CGCCCAGTGG	CTCGACGTTC	TTGAGAAGGA	GTGCGCGCAG	
3351	AGCCGTTCCA	CACCCAGCGC		GGCGCCACCG	CCAGACCTGG
3401	TGCGGCCTCT	CGCAGCTTCG	CCCCCGCCAC	AAGCGGCTCT	TCGGCCCGCG AGCCGGGCGC
3451	GTACCGGCTC	AACTCGCCAA	GGGCCGACCG	GCGCGTCGTT	CAGATGGAAG GTCTACCTTC
3501	CGGAGGACCG	CGGCGTGGCC	GGGTTCCTCG	GGCGCACCAA	CCTGGCCACC GGACCGGTGG
3551	CAGCCGCAGA	GCGGGCTGGT	GGTCCCGTTC	CCAGACCCGT	GCGCCGTCGT CGCGGCAGCA
3601	CGAGGGGCCT	CACCTCCGCC	GGCTCGCGCG	GCCCCACGGG	GCCTTCCTGG GCGAAGGACC
3651	TCTGGAGGCG	CGGGGCGTTG	GAGGGGAAGA	TGCTCGCCGA	CGGCTTCACC CGCGAAGTGG
3701	CAGTGGCGGC	TGCAGCTCAC	GGGCTTCCTG	GCGCGCTGGA	GGTGCATGAC CCACGTACTG
3751	GGCGTTCGGG	G CCACGGACTG	CGGGCGGGT	GCTGGGCGTC	GCCCCGACCG GCGGGCTGGC
3801	TTTCCTCGCC	G TGCTGGGGTA	CCGAGGCTGG	CTTCGGCTGC	C CGGGCGGCCC G GCCCGCGGG
3851					ACTCGAGATC TGAGCTCTAG

3901		CTCTGGATTA GAGACCTAAT			
3951		GCTCCTTTTA			
J J J I		CGAGGAAAAT			
4001	TGTATCATGC	TATTGCTTCC	CGTATGGCTT	TCATTTTCTC	CTCCTTGTAT
	ACATAGTACG	ATAACGAAGG	GCATACCGAA	AGTAAAAGAG	GAGGAACATA
4051	AAATCCTGGT	TGCTGTCTCT	TTATGAGGAG	TTGTGGCCCG	TTGTCAGGCA
	TTTAGGACCA	ACGACAGAGA	AATACTCCTC	AACACCGGGC	AACAGTCCGT
4101	ACGTGGCGTG	GTGTGCACTG	TGTTTGCTGA	CGCAACCCCC	ACTGGTTGGG
	TGCACCGCAC	CACACGTGAC	ACAAACGACT	$\tt GCGTTGGGGG$	TGACCAACCC
4151	GCATTGCCAC	CACCTGTCAG	CTCCTTTCCG	${\tt GGACTTTCGC}$	TTTCCCCCTC
	CGTAACGGTG	GTGGACAGTC	GAGGAAAGGC	CCTGAAAGCG	AAAGGGGGAG
4201	CCTATTGCCA	CGGCGGAACT	CATCGCCGCC	${\tt TGCCTTGCCC}$	GCTGCTGGAC
	GGATAACGGT	GCCGCCTTGA	GTAGCGGCGG	ACGGAACGGG	CGACGACCTG
4251	AGGGGCTCGG	CTGTTGGGCA	${\tt CTGACAATTC}$	${\tt CGTGGTGTTG}$	TCGGGGAAAT
	TCCCCGAGCC	GACAACCCGT	GACTGTTAAG	GCACCACAAC	AGCCCCTTTA
4301	CATCGTCCTT	TCCTTGGCTG	$\mathtt{CTCGCCTGTG}$	TTGCCACCTG	GATTCTGCGC
	GTAGCAGGAA	AGGAACCGAC	GAGCGGACAC	AACGGTGGAC	CTAAGACGCG
4351	GGGACGTCCT	TCTGCTACGT	CCCTTCGGCC	CTCAATCCAG	CGGACCTTCC
	CCCTGCAGGA	AGACGATGCA	GGGAAGCCGG	GAGTTAGGTC	GCCTGGAAGG
4401		CTGCTGCCGG			
	AAGGGCGCCG	GACGACGGCC	GAGACGCCGG	AGAAGGCGCA	GAAGCGGAAG
4451		GAGTCGGATC			
		CTCAGCCTAG			
4501		GCTGATCAGC			
	AGATCTCGAG	CGACTAGTCG	GAGCTGACAC	GGAAGATCAA	CGGTCGGTAG
4551		CCCTCCCCCG			
		GGGAGGGGC			
4601		TTCCTAATAA			
					AACAGACTCA
4651					GCAAGGGGGA
					CGTTCCCCCT
4701					GGCTCTATGG
					CCGAGATACC
4751					CTAGTTGTGG
4004					GATCAACACC
4801					CCGTCGACCT GGCAGCTGGA
4051					TGTGTGAAAT
4851					ACACACTTTA
4001					GCATAAAGTG
4901					CGTATTTCAC
40E1					ATTGCGTTGC
4951					TAACGCAACG
5001					GCTGCATTAA
2001					CGACGTAATT

FIGURE 9-5

5051	man nmaaaaa	A A CCCCCCCCC	CACACCCC	mmcccm a mmc	aaaaamamma
3031		AACGCGCGGG TTGCGCGCCC			
5101		CTCACTGACT			
3101		GAGTGACTGA			
5151		TCACTCAAAG			
		AGTGAGTTTC			
5201	GATAACGCAG	GAAAGAACAT	GTGAGCAAAA	GGCCAGCAAA	AGGCCAGGAA
	CTATTGCGTC	CTTTCTTGTA	CACTCGTTTT	CCGGTCGTTT	TCCGGTCCTT
5251	CCGTAAAAAG	GCCGCGTTGC	TGGCGTTTTT	CCATAGGCTC	CGCCCCCTG
	${\tt GGCATTTTTC}$	CGGCGCAACG	ACCGCAAAAA	GGTATCCGAG	GCGGGGGGAC
5301	ACGAGCATCA	${\tt CAAAAATCGA}$	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA
	TGCTCGTAGT	GTTTTTAGCT	GCGAGTTCAG	TCTCCACCGC	TTTGGGCTGT
5351		GATACCAGGC			
		CTATGGTCCG			
5401		ACCCTGCCGC			
- 4		TGGGACGGCG			
5451		GGCGCTTTCT			
EE01		CCGCGAAAGA			
5501		TTCGCTCCAA AAGCGAGGTT			
5551		TGCGCCTTAT			
3331		ACGCGGAATA			
5601		CTTATCGCCA			
		GAATAGCGGT			
5651	AGAGCGAGGT	ATGTAGGCGG	TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA
•	TCTCGCTCCA	TACATCCGCC	ACGATGTCTC	AAGAACTTCA	CCACCGGATT
5701	CTACGGCTAC	ACTAGAAGGA	CAGTATTTGG	TATCTGCGCT	CTGCTGAAGC
	GATGCCGATG	TGATCTTCCT	GTCATAAACC	ATAGACGCGA	GACGACTTCG
5751	CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	CAAACAAACC
		GCCTTTTTCT			
5801		GCGGTGGTTT			
5054		CGCCACCAAA			
5851		TCTCAAGAAG AGAGTTCTTC			
5901					
2901					GAGATTATCA CTCTAATAGT
5951		TCACCTAGAT			
37 31					CAAAATTTAG
6001					CAATGCTTAA
					GTTACGAATT
6051					ATCCATAGTT
					TAGGTATCAA
6101	GCCTGACTCC	CCGTCGTGTA	GATAACTACG	ATACGGGAGG	GCTTACCATC
	CGGACTGAGG	GGCAGCACAT	CTATTGATGC	TATGCCCTCC	CGAATGGTAG
6151	TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	CCCACGCTCA	CCGGCTCCAG
	ACCGGGGTCA	CGACGTTACT	ATGGCGCTCT	GGGTGCGAGT	GGCCGAGGTC

FIGURE 9-6

6201			CCAGCCGGAA GGTCGGCCTT		
6251			CATCCAGTCT		
	GGACGTTGAA	ATAGGCGGAG	GTAGGTCAGA	TAATTAACAA	CGGCCCTTCG
6301	TAGAGTAAGT	AGTTCGCCAG	TTAATAGTTT	GCGCAACGTT	GTTGCCATTG
	ATCTCATTCA	TCAAGCGGTC	AATTATCAAA	CGCGTTGCAA	CAACGGTAAC
6351	CTACAGGCAT	${\tt CGTGGTGTCA}$	${\tt CGCTCGTCGT}$	${\tt TTGGTATGGC}$	TTCATTCAGC
	GATGTCCGTA	GCACCACAGT	GCGAGCAGCA	AACCATACCG	AAGTAAGTCG
6401	TCCGGTTCCC	AACGATCAAG	$\tt GCGAGTTACA$	TGATCCCCCA	TGTTGTGCAA
	AGGCCAAGGG	TTGCTAGTTC	CGCTCAATGT	ACTAGGGGGT	ACAACACGTT
6451	AAAAGCGGTT	${\tt AGCTCCTTCG}$	${\tt GTCCTCCGAT}$	CGTTGTCAGA	AGTAAGTTGG
	TTTTCGCCAA	TCGAGGAAGC	CAGGAGGCTA	GCAACAGTCT	TCATTCAACC
6501	CCGCAGTGTT	ATCACTCATG	GTTATGGCAG	CACTGCATAA	TTCTCTTACT
	GGCGTCACAA	TAGTGAGTAC	CAATACCGTC	GTGACGTATT	AAGAGAATGA
6551			CTTTTCTGTG		
	CAGTACGGTA	GGCATTCTAC	GAAAAGACAC	TGACCACTCA	TGAGTTGGTT
6601	GTCATTCTGA	GAATAGTGTA	TGCGGCGACC	GAGTTGCTCT	TGCCCGGCGT
	CAGTAAGACT	CTTATCACAT	ACGCCGCTGG	CTCAACGAGA	ACGGGCCGCA
6651			CCACATAGCA		
	GTTATGCCCT	ATTATGGCGC	GGTGTATCGT	CTTGAAATTT	TCACGAGTAG
6701			GCGAAAACTC		
	TAACCTTTTG	CAAGAAGCCC	CGCTTTTGAG	AGTTCCTAGA	ATGGCGACAA
6751	0110111 0 0110 1		CCACTCGTGC		
	CTCTAGGTCA	AGCTACATTG	GGTGAGCACG	TGGGTTGACT	AGAAGTCGTA
6801	*		TCTGGGTGAG		
	GAAAATGAAA	GTGGTCGCAA	AGACCCACTC	GTTTTTGTCC	TTCCGTTTTA
6851			GGCGACACGG		
	CGGCGTTTTT	TCCCTTATTC	CCGCTGTGCC	TTTACAACTT	ATGAGTATGA
6901					TGTCTCATGA
	GAAGGAAAAA	GTTATAATAA	CTTCGTAAAT	AGTCCCAATA	ACAGAGTACT
6951					AGGGGTTCCG
	CGCCTATGTA	TAAACTTACA	TAAATCTTTT	TATTTGTTTA	TCCCCAAGGC
7001			GCCACCTGAC		
	GCGTGTAAAG	GGGCTTTTCA	CGGTGGACTG	CAG	

FIG. 10 (1-12)

pCEP4W/hepEK

1	TCGAGCGGCC GCTTTAAACT CA	ATGGTGAT	GGTGATGATG	ACCGGTACGC
	AGCTCGCCGG CGAAATTTGA GT	TACCACTA	CCACTACTAC	TGGCCATGCG
-3		н н н	н н н	GTRT
51	GTAGAATCGA GACCGAGGAG AG	GGTTAGGG	ATAGGCTTAC	CGAATTCGAG
	CATCTTAGCT CTGGCTCCTC TC	CCAATCCC	TATCCGAATG	GCTTAAGCTC
-3	·TSDLGLLF	N P	I P K G	FEL
101	CTGGGTCACC ATGCCGCTGG CT	TCGGAGTG	AGTCTTTATG	GCCTGGAAGA
	GACCCAGTGG TACGGCGACC GA	AGCCTCAC	TCAGAAATAC	CGGACCTTCT
-3	Q T V M G S A	E S H	TKI	A Q F I
151	TCCACTCCCG GAAGTCACTG AC	CTTTGGTGT	AGACGCCTGG	CTTCTGGGCC
	AGGTGAGGGC CTTCAGTGAC TO	GAAACCACA	TCTGCGGACC	GAAGACCCGG
-3	·IW E R F D S V	K T Y	V G P	KQAL
201	AGGGCACAGC CAGTGCCCCA AC	CTCACAATG	CCACACAGCC	GCCAACGTGG
	TCCCGTGTCG GTCACGGGGT TC	GAGTGTTAC	GGTGTGTCGG	CGGTTGCACC
-3	·LACGTGW	8 V I	G C L R	WRP
251	CGTCCGAGAG ATGCTGTCCT CA	ACACACAAA	GGGACCACCG	CTGTCGCCCT
	GCAGGCTCTC TACGACAGGA GT	rgtgtgttt	CCCTGGTGGC	GACAGCGGGA
-3	TRSISDE	C V F	P G G	S D G Q.
301	GGCAGGCATC AATGCCACCC TO		CAGCACAGAA	
	CCGTCCGTAG TTACGGTGGG AC	GCCCCATCG	GTCGTGTCTT	GTAGAACCCG
-3	·QCADIGGE	PΥG	A C F	M K P K
351	TTGATCTGGT TTCCATAGAA A	TCAGCGCCA	TTGCAGACAT	CATTGCTGAT
	AACTAGACCA AAGGTATCTT T	AGTCGCGGT	AACGTCTGTA	GTAACGACTA
-3	·KIQNGYFI	D A G	N C V D	N S 1
401	TATGGGGACT CGAGCCTCCT G	GAGTACCCC	GGCCTGTTGG	CCATAGTACT
	ATACCCCTGA GCTCGGAGGA C	CTCATGGGG	CCGGACAACC	GGTATCATGA
-3	IPVRAEQ	L V G	A Q Q	G Y Y Q.
451			TCTTGCCATC	CACCAGGGCC
	CGCACAACGG GGTCGGGCAG T	GCCATGTCT	AGAACGGTAG	GTGGTCCCGG
-3	·Q T N G W G T V	TCI	K G D	V L A Q
501	TGGCCGGCAG CTGGGAGGCA C	ACAGGCTGG	ATGTATTCTG	TGAGGGGCAG
	ACCGGCCGTC GACCCTCCGT G	TGTCCGACC	TACATAAGAC	ACTCCCCGTC
-3	·Q G A A P L C	V P Q	IYET	LPL
551	GGGACTGGAG AGGTGGACCA G			TCCTCGCTGT
	CCCTGACCTC TCCACCTGGT C	CCGTTATAG	CAACGACAAG	AGGAGCGACA
-3	PSS L H V Ł	A I D	N S N	E S N.
601	TGGGGTCCCG AAAGGGAAGA T			
	ACCCCAGGGC TTTCCCTTCT A	TCGGGGGCA	CCATCTGGTG	TCGGACGTGG
-3	·NPDRFPLY	GGH	HYVV	A Q V G
651	CCCAGCTGCA GACCGTGGGG A			
	GGGTCGACGT CTGGCACCCC T	CTCCGGACC		
-3		S A Q	AVAC	
701	TCGCCATCGG GACAGGACCC G			
	AGCGGTAGCC CTGTCCTGGG C	**		
-3	RWRSLVR	N R E	PFC	H A A T

FIGUREIO-1

١

751 TCAGCACCCA GTCCCCGGAG AGCAGGGATC CCCCACAGAG GTGTGCTCCA AGTCGTGGGT CAGGGGCCTC TCGTCCCTAG GGGGTGTCTC CACACGAGGT -3 ·TLV W D G S L L S G G C L H A G D 801 TCATAGCGAA GGCTGACTTG CCACGGCCAC CGGCCCAAGC TGGTGTCCCG AGTATCGCTT CCGACTGAAC GGTGCCGGTG GCCGGGTTCG ACCACAGGGC ·DYRLSVQWPWRGL 851 GCCTCCCACG ATCTTGTCGT CGTCGTCCAC GGGCAGCTTC CTGCGGCCAC CGGAGGTGC TAGAACAGCA GCAGCAGGTG CCCGTCGAAG GACGCCGGTG G G V I K D D D D V P Ł K R R G C · 901 AGTCTTGGCA GATGGCGGCC AAGAAACGGC CTCTGGGGCA ATCACACACG TCAGAACCGT CTACCGCCGG TTCTTTGCCG GAGACCCCGT TAGTGTGTGC -3 · C D Q C I A A L F R G R P C D C V S 951 GAGATGACCT CCAGCAGCCT CTGGGTGTGG GGCAGCCTCC CCTCGTCCAC CTCTACTGGA GGTCGTCGGA GACCCACACC CCGTCGGAGG GGAGCAGGTG SIVELLRQTHPLRGEDV ACAGAAGAAG CCCGACGTGC CATTGGCGCC CGCCGTTCGC ACGTCCAGCT 1001 TGTCTTCTTC GGGCTGCACG GTAACCGCGG GCGGCAAGCG TGCAGGTCGA CFFGSTGNAGATR CGGAGTGGGT CAGTGCCCTG AGGAAGCCCA TCTCCTCGCA GCTGAGTCCG 1051 GCCTCACCCA GTCACGGGAC TCCTTCGGGT AGAGGAGCGT CGACTCAGGC -3 ·ESHTLARLFGMEECSLGA GCTACCCTGG CGTTAGAGCG CGAGGAGCAC AGCAGCCGCC ACGTCCCTTC 1101 CGATGGGACC GCAATCTCGC GCTCCTCGTG TCGTCGGCGG TGCAGGGAAG · A V R A N S R S S C Ł L R W T G CGTCTTGTCA AAGACCATGA GCCGAGCGTC CGCAGAGCTG ACCTGCACTG 1151 GCAGAACAGT TTCTGGTACT CGGCTCGCAG GCGTCTCGAC TGGACGTGAC T K D F V M L R A D A S S V Q V P· GGTACAGCGG CTCCTGGTCA CTCCTATCCG GAGCGTCACC AGTGGAACCT 1201 CCATGTCGCC GAGGACCAGT GAGGATAGGC CTCGCAGTGG TCACCTTGGA EQDSRDP GGAACCCAGA GCAGCAGTAC CCATAGCAGG AGTGTGTCTG TCTCCATGGT 1251 CCTTGGGTCT CGTCGTCATG GGTATCGTCC TCACACAGAC AGAGGTACCA PVWLLLVWLLETDTEM GGCGATCTGG TACCCAGCTT CTAGAGATCT GACGGTTCAC TAAACGAGCT 1301 CCGCTAGACC ATGGGTCGAA GATCTCTAGA CTGCCAAGTG ATTTGCTCGA CTGCTTATAT AGACCTCCCA CCGTACACGC CTACCGCCCA TTTGCGTCAA 1351 GACGAATATA TCTGGAGGGT GGCATGTGCG GATGGCGGGT AAACGCAGTT 1401 CGGGGCGGG TTATTACGAC ATTTTGGAAA GTCCCGTTGA TTTTGGTGCC GCCCCGCCC AATAATGCTG TAAAACCTTT CAGGGCAACT AAAACCACGG AAAACAAACT CCCATTGACG TCAATGGGGT GGAGACTTGG AAATCCCCGT 1451 TTTTGTTTGA GGGTAACTGC AGTTACCCCA CCTCTGAACC TTTAGGGGCA GAGTCAAACC GCTATCCACG CCCATTGGTG TACTGCCAAA ACCGCATCAC 1501 CTCAGTTTGG CGATAGGTGC GGGTAACCAC ATGACGGTTT TGGCGTAGTG 1551 CATGGTAATA GCGATGACTA ATACGTAGAT GTACTGCCAA GTAGGAAAGT GTACCATTAT CGCTACTGAT TATGCATCTA CATGACGGTT CATCCTTTCA

1601		CATGTACTGG			
		GTACATGACC			
1651		TAGGGGGGGG			
		ATCCCCCGCC			
1701		GTTTACCGTA			
		CAAATGGCAT			
1751		CGTTACTATG			
		GCAATGATAC			
1801		TGGGCGGTCA			
		ACCCGCCAGT			
1851		TCCATATATG			
4004		AGGTATATAC			
1901	· -	ACTAGTCAAT			
4054		TGATCAGTTA			
1951	-	TATAAATGTA ATATTTACAT			
0001					
2001		CCAATATTGA			
0051		GGTTATAACT			
2051		ATATTGATTC TATAACTAAG			
0101					
2101		GCAATGCAAC CGTTACGTTG			
2151					
2151		GAATTGGTCG CTTAACCAGC			
2201					
2201		GGGTCGGGGG			
2251		GTACATGCGG			
2251		CATGTACGCC			
2301					CGCCCAAAAT
2301					GCGGGTTTTA
2351					CCCGTCCCTA
2331					GGGCAGGGAT
2401					ACGTTGGCTG
2401					TGCAACCGAC
2451					GGAAAAGGAA
2471					CCTTTTCCTT
2501					TATCGACAGA
2301					ATAGCTGTCT
2551	GTGCCAGCCC	TGGGACCGAA	CCCCGCGTTT	ATGAACAAAC	GACCCAACAC
					CTGGGTTGTG
2601	CCGTGCGTTT	TATTCTGTCT	TTTTATTGCC	GTCATAGCGC	GGGTTCCTTC
-	GGCACGCAAA	ATAAGACAGA	AAAATAACGG	CAGTATCGCG	CCCAAGGAAG
2651	CGGTATTGTC	TCCTTCCGTG	TTTCAGTTAG	CCTCCCCCAT	CTCCCCTATT
•					GAGGGGATAA
2701	CCTTTGCCCT	CGGACGAGTG	CTGGGGCGTC	GGTTTCCACT	ATCGGCGAGT
	GGAAACGGGA	GCCTGCTCAC	GACCCCGCAG	CCAAAGGTGA	TAGCCGCTCA

2751				GCGCTTCTGC CGCGAAGACG	
0001	_				
2801				GACGATTGCG CTGCTAACGC	
2851	CCTGCGCCCA	AGCTGCATCA	TCGAAATTGC	CGTCAACCAA	GCTCTGATAG
	GGACGCGGGT	TCGACGTAGT	AGCTTTAACG	GCAGTTGGTT	CGAGACTATC
2901	AGTTGGTCAA	GACCAATGCG	GAGCATATAC	GCCCGGAGCC	GCGGCGATCC
				CGGGCCTCGG	
2951	TGCAAGCTCC	GGATGCCTCC	GCTCGAAGTA	GCGCGTCTGC	TGCTCCATAC
	ACGTTCGAGG	CCTACGGAGG	CGAGCTTCAT	CGCGCAGACG	ACGAGGTATG
3001	AAGCCAACCA	CGGCCTCCAG	AAGAAGATGT	TGGCGACCTC	GTATTGGGAA
	TTCGGTTGGT	GCCGGAGGTC	${\tt TTCTTCTACA}$	ACCGCTGGAG	CATAACCCTT
3051	TCCCCGAACA	TCGCCTCGCT	CCAGTCAATG	ACCGCTGTTA	TGCGGCCATT
	AGGGGCTTGT	AGCGGAGCGA	GGTCAGTTAC	TGGCGACAAT	ACGCCGGTAA
3101	GTCCGTCAGG	ACATTGTTGG	AGCCGAAATC	CGCGTGCACG	AGGTGCCGGA
	CAGGCAGTCC	TGTAACAACC	TCGGCTTTAG	GCGCACGTGC	TCCACGGCCT
3151	CTTCGGGGCA	GTCCTCGGCC	CAAAGCATCA	GCTCATCGAG	AGCCTGCGCG
	GAAGCCCCGT	CAGGAGCCGG	GTTTCGTAGT	CGAGTAGCTC	TCGGACGCGC
3201	ACGGACGCAC	TGACGGTGTC	GTCCATCACA	GTTTGCCAGT	GATACACATG
	TGCCTGCGTG	ACTGCCACAG	CAGGTAGTGT	CAAACGGTCA	CTATGTGTAC
3251	GGGATCAGCA	ATCGCGCATA	TGAAATCACG	CCATGTAGTG	TATTGACCGA
	CCCTAGTCGT	TAGCGCGTAT	ACTTTAGTGC	GGTACATCAC	ATAACTGGCT
3301	TTCCTTGCGG	TCCGAATGGG	CCGAACCCGC	TCGTCTGGCT	AAGATCGGCC
	AAGGAACGCC	AGGCTTACCC	GGCTTGGGCG	AGCAGACCGA	TTCTAGCCGG
3351				GGCTGCAGAA	
	CGTCGCTAGC	GTAGGTACCG	GAGGCGCTGG	CCGACGTCTT	GTCGCCCGTC
3401				ACCCTGTGCA	
	AAGCCAAAGT	CCGTCCAGAA	CGTTGCACTG	TGGGACACGT	GCCGCCCTCT
3451					CACTTCCGGA
	ACGTTATCCA	GTCCGAGAGC	GACTTAAGGG	GTTACAGTTC	GTGAAGGCCT
3501					GATCTTTGTA
					CTAGAAACAT
3551					CGCCCTCCTA
					GCGGGAGGAT
3601					CTGCATCAGG
					GACGTAGTCC
3651					CAGACGTCGC
					GTCTGCAGCG
3701					GCGGCACGCT
					CGCCGTGCGA
3751					TTCGAGGCCA
					AAGCTCCGGT
3801					CCGCCCCGAC
					GGCGGGGCTG
3851					GCGGGGTTTG
	ACGTAGACG	C ACAAGCTTAA	A GCGGTTACTO	TTCTGCGACC	CCCCCAAAC

3901			CATGCAAATA GTACGTTTAT		
3951			GCCACGGGGA CGGTGCCCCT		
4001	GACGCGCTGG	GCTACGTCTT	GCTGGCGTTC CGACCGCAAG	GCGACGCGAG	GCTGGATGGC
4051	CTTCCCCATT	ATGATTCTTC	TCGCTTCCGG AGCGAAGGCC	CGGCATCGGG	ATGCCCGCGT
4101	TGCAGGCCAT	GCTGTCCAGG	CAGGTAGATG GTCCATCTAC	ACGACCATCA	GGGACAGCTT
4151	CAAGGATCGC	TCGCGGCTCT	TACCAGCCTA ATGGTCGGAT	ACTTCGATCA	CTGGACCGCT
4201	GATCGTCACG	GCGATTTATG	CCGCCTCGGC GGCGGAGCCG	GAGCACATGG	AACGGGTTGG
4251	CATGGATTGT	AGGCGCCGCC	CTATACCTTG GATATGGAAC	TCTGCCTCCC	CGCGTTGCGT
4301	CGCGGTGCAT	GGAGCCGGGC	CACCTCGACC GTGGAGCTGG	TGAATGGAAG	CCGGCGGCAC
4351	CTCGCTAACG	GATTCACCAC	TCCAAGAATT AGGTTCTTAA	GGAGCCAATC	AATTCTTGCG
4401	GAGAACTGTG	AATGCGCAAA	CCAACCCTTG GGTTGGGAAC	GCAGAACATA	TCCATCGCGT
4451			ACGCGGCGCA TGCGCCGCGT		AGGAACCGTA TCCTTGGCAT
4501			TTTTTCCATA AAAAAGGTAT		
4551					CGACAGGACT GCTGTCCTGA
4601					CGCTCTCCTG GCGAGAGGAC
4651					CCCTTCGGGA GGGAAGCCCT
4701					GTTCGGTGTA CAAGCCACAT
4751					GTTCAGCCCG CAAGTCGGGC
4801					CCCGGTAAGA GGGCCATTCT
4851					TTAGCAGAGC AATCGTCTCG
4901					G CCTAACTACG C GGATTGATGC
4951					r GAAGCCAGTT A CTTCGGTCAA
5001					C AAACCACCGC G TTTGGTGGCG

5051		GGTTTTTTTG CCAAAAAAAC			
F101		AGAAGATCCT			
5101		TCTTCTAGGA			
5151	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG
	ACCTTGCTTT	TGAGTGCAAT	TCCCTAAAAC	CAGTACTCTA	ATAGTTTTTC
5201	GATCTTCACC	TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT
	CTAGAAGTGG	ATCTAGGAAA	ATTTAATTTT	TACTTCAÀAA	TTTAGTTAGA
5251	AAAGTATATA	TGAGTAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT
	TTTCATATAT	ACTCATTTGA	ACCAGACTGT	CAATGGTTAC	GAATTAGTCA
5301	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	CGTTCATCCA	TAGTTGCCTG
	CTCCGTGGAT	AGAGTCGCTA	GACAGATAAA	GCAAGTAGGT	ATCAACGGAC
5351	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	CCATCTGGCC
		CACATCTATT			
5401	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	TCCAGATTTA
3 20 2		TTACTATGGC			
5451	TCAGCAATAA	ACCAGCCAGC	CGGAAGGCC	GAGCGCAGAA	GTGGTCCTGC
0 10 1		TGGTCGGTCG			
5501	AACTTTATCC	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG
0002		CGGAGGTAGG			
5551	ТААСТАСТТС	GCCAGTTAAT	AGTTTGCGCA	ACGTTGTTGC	CATTGCTGCA
3331	ATTCATCAAG	CGGTCAATTA	TCAAACGCGT	TGCAACAACG	GTAACGACGT
5601	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	ATGGCTTCAT	TCAGCTCCGG
3001		ACAGTGCGAG			
5651	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	TGCAAAAAAG
3031		AGTTCCGCTC			
5701	СССТТАССТС	CTTCGGTCCT	СССАТССТТС	TCAGAAGTAA	GTTGGCCGCA
3,01		GAAGCCAGGA			
5751		TCATGGTTAT			
3,31		AGTACCAATA			
5801	GCCATCCGTA	AGATGCTTTT	СТСТСАСТСС	ТСАСТАСТСА	ACCAAGTCAT
3001		TCTACGAAAA			
5851	ТСТСАСААТА	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	GGCGTCAACA
0002		CACATACGCC			
5901	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	TCATCATTGG
	GCCCTATTAT	GGCGCGGTGT	ATCGTCTTGA	AATTTTCACG	AGTAGTAACC
5951	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	CTGTTGAGAT
	TTTTGCAAGA	AGCCCCGCTT	TTGAGAGTTC	CTAGAATGGC	GACAACTCTA
6001	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	AGCATCTTTT
					TCGTAGAAAA
6051	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC
		CGCAAAGACC			
6101	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC
					TATGAGAAGG
6151	TTTTTCAATA	TTATTGAAGC	ATTTATCAGG	GTTATTGTCT	CATGAGCGGA
					GTACTCGCCT

6201			GAAAAATAAA		
	ATGTATAAAC	TTACATAAAT	CTTTTTATTT	GTTTATCCCC	AAGGCGCGTG
6251			CTGACGTCTA		
			GACTGCAGAT		
6301			CGTATCACGA		-0-10-10-11
			GCATAGTGCT		
6351			TCATCGATAA		
C 4 0 4			AGTAGCTATT		
6401			CCCAGTAGCA		
C 4 E 1			GGGTCATCGT		
6451			GAGAATCCCC		
CE 01			CTCTTAGGGG		
6501			GCCTGGCTTG		
6551			CGGACCGAAC		
0221			TTCCGGGCTG AAGGCCCGAC		
6601			GGGAATTTTC		
0001			CCCTTAAAAG		
6651			GGTGGGGGG		
0031			CCACCCCCC		
6701			GAGCGTCGTC		
0,01			CTCGCAGCAG		
6751			TCTGACGAGG		
			AGACTGCTCC		
6801	AATGGCCTAG	GAGAGAAGGG	AGACACATCT	GGACCAGAAG	GCTCCGGCGG
			TCTGTGTAGA		
6851	CAGTGGACCT	CAAAGAAGAG	GGGGTGATAA	CCATGGACGA	GGACGGGGAA
			CCCCACTATT		
6901	GAGGACGAGG	ACGAGGAGGC	GGAAGACCAG	GAGCCCCGGG	CGGCTCAGGA
	CTCCTGCTCC	TGCTCCTCCG	CCTTCTGGTC	CTCGGGGCCC	GCCGAGTCCT
6951	TCAGGGCCAA	GACATAGAGA	TGGTGTCCGG	AGACCCCAAA	AACGTCCAAG
	AGTCCCGGTT	CTGTATCTCT	ACCACAGGCC	TCTGGGGTTT	TTGCAGGTTC
7001	TTGCATTGGC	TGCAAAGGGA	CCCACGGTGG	AACAGGAGCA	GGAGCAGGAG
	AACGTAACCG	ACGTTTCCCT	GGGTGCCACC	TTGTCCTCGT	CCTCGTCCTC
7051			GGGGCAGGAG		
	GCCCTCCCCG	TCCTCGTCCT	CCCCGTCCTC	GTCCTCCTCC	CCGTCCTCGT
7101	GGAGGAGGG	CAGGAGGGC	AGGAGGGCA	GGAGGGGCAG	GAGCAGGAGG
	CCTCCTCCCC	GTCCTCCCCG	TCCTCCCCGT	CCTCCCCGTC	CTCGTCCTCC
7151					GCAGGAGCAG
	TCCCCGTCCT	CGTCCTCCTC	CCCGTCCTCC	CCGTCCTCCC	CGTCCTCGTC
7201					AGCAGGAGGA
					TCGTCCTCCT
7251					CAGGAGCAGG
					GTCCTCGTCC
7301					GGGGCAGGAG
	TCCTCCCCGT	CCTCCCCGTC	CTCGTCCTCC	TCCCCGTCCT	CCCCGTCCTC

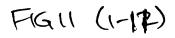
7351		AGGAGGAGGG TCCTCCTCCC			
7401		CAGGAGGGC			
	CCCCGTCCTC	GTCCTCCCCG	TCCTCGTCCT	CCTCCCCGTC	CTCCCCGTCC
7451		GCAGGAGGGG CGTCCTCCCC			
7501		AGGGGCAGGA			
	GTCCTCGTCC	TCCCCGTCCT	CCCCGTCCTC	GTCCTCCCCG	TCCTCCCGT
7551		GGGCAGGAGG			
	CCTCGTCCTC	CCCGTCCTCC	CCGTCCTCGT	CCTCCTCCCC	GTCCTCCCCG
7601		GGAGGGGCAG			
	TCCTCGTCCT	CCTCCCCGTC	CTCCCCGTCC	TCGTCCTCCC	CGTCCTCCCC
7651		AGGGGCAGGA			
	GTCCTCGTCC	TCCCCGTCCT	CCCCGTCCTC	GTCCTCCCCG	TCCTCCCCGT
7701	GGAGCAGGAG	GAGGGCAGG	AGCAGGAGGG	GCAGGAGCAG	GAGGTGGAGG
		CTCCCCGTCC			
7751	CCGGGGTCGA	GGAGGCAGTG	GAGGCCGGGG	TCGAGGAGGT	AGTGGAGGCC
	GGCCCCAGCT	CCTCCGTCAC	CTCCGGCCCC	AGCTCCTCCA	TCACCTCCGG
7801	GGGGTCGAGG	AGGTAGTGGA	GGCCGCCGGG	GTAGAGGACG	TGAAAGAGCC
	CCCCAGCTCC	TCCATCACCT	CCGGCGGCCC	CATCTCCTGC	ACTTTCTCGG
7851	AGGGGGGAA	GTCGTGAAAG	AGCCAGGGGG	AGAGGTCGTG	GACGTGGAGA
	TCCCCCCTT	CAGCACTTTC	TCGGTCCCCC	TCTCCAGCAC	CTGCACCTCT
7901		AGGAGTCCCA			
		TCCTCAGGGT			
7951	CGCGCAGGCC	CCCTCCAGGT	AGAAGGCCAT	TTTTCCACCC	TGTAGGGGAA
		$\tt GGGAGGTCCA$			
8001		TTGAATACCA			
	CGGCTAATAA	AACTTATGGT	GGTTCTTCCA	CCGGGTCTAC	CACTCGGACT
8051		GGAGCGATAG			
	GCACGGGGGC	CCTCGCTATC	TCGTCCCGGG	GCGTCTACTG	GGTCCTCTTC
8101	GCCCAAGCAC	TGGACCCCGG	GGTCAGGGTG	ATGGAGGCAG	GCGCAAAAA
	CGGGTTCGTG	ACCTGGGGCC	CCAGTCCCAC	TACCTCCGTC	CGCGTTTTTT
8151		TTGGAAAGCA			
		AACCTTTCGT			
8201	TGAGAACATT	GCAGAAGGTT	TAAGAGCTCT	CCTGGCTAGG	AGTCACGTAG
	ACTCTTGTAA	CGTCTTCCAA	ATTCTCGAGA	GGACCGATCC	TCAGTGCATC
8251	AAAGGACTAC	CGACGAAGGA	ACTTGGGTCG	CCGGTGTGTT	CGTATATGGA
		GCTGCTTCCT			
8301		CCTCCCTTTA			
	CCATCATTCT	GGAGGGAAAT	GTTGGATTCC	GCTCCTTGAC	GGGAACGATA
8351		CGTCTTACAC			
		GCAGAATGTG			
8401		CCCACAACCT			
	GACCTGGGCC	GGGTGTTGGA	CCGGGCGATT	CCCTCAGGTA	ACAGACAATA
8451		TTTTACAAAC			
	AAGTACCAGA	AAAATGTTTG	AGTATATAAA	CGACTCCAAA	ACTTCCTACG

8501		CTTGTTATGA			
		GAACAATACT			
8551		CAGCTTTGAC			
		GTCGAAACTG			
8601		AAGGGGCTGC			
	GGATACCACC	TTCCCCGACG	GCGCCTCCCA	CTACTGCCTC	TACTGCCTCT
8651	TGAAGGAGGT	GATGGAGATG	AGGGTGAGGA	AGGGCAGGAG	TGATGTAACT
	ACTTCCTCCA	CTACCTCTAC	TCCCACTCCT	TCCCGTCCTC	ACTACATTGA
8701	TGTTAGGAGA	CGCCCTCAAT	CGTATTAAAA	GCCGTGTATT	CCCCCGCACT
	ACAATCCTCT	GCGGGAGTTA	${\tt GCATAATTTT}$	CGGCACATAA	GGGGGCGTGA
8751	AAAGAATAAA	TCCCCAGTAG	ACATCATGCG	TGCTGTTGGT	GTATTTCTGG
	TTTCTTATTT	AGGGGTCATC	TGTAGTACGC	ACGACAACCA	CATAAAGACC
8801	CCATCTGTCT	TGTCACCATT	TTCGTCCTCC	CAACATGGGG	CAATTGGGCA
	GGTAGACAGA	ACAGTGGTAA	AAGCAGGAGG	GTTGTACCCC	GTTAACCCGT
8851	TACCCATGTT	GTCACGTCAC	TCAGCTCCGC	GCTCAACACC	TTCTCGCGTT
	ATGGGTACAA	CAGTGCAGTG	AGTCGAGGCG	CGAGTTGTGG	AAGAGCGCAA
8901	GGAAAACATT	AGCGACATTT	ACCTGGTGAG	CAATCAGACA	TGCGACGGCT
	CCTTTTGTAA	TCGCTGTAAA	TGGACCACTC	GTTAGTCTGT	ACGCTGCCGA
8951	TTAGCCTGGC	CTCCTTAAAT	TCACCTAAGA	ATGGGAGCAA	CCAGCATGCA
	AATCGGACCG	GAGGAATTTA	AGTGGATTCT	TACCCTCGTT	GGTCGTACGT
9001	GGAAAAGGAC	AAGCAGCGAA	AATTCACGCC	CCCTTGGGAG	GTGGCGGCAT
	CCTTTTCCTG	${\tt TTCGTCGCTT}$	TTAAGTGCGG	GGGAACCCTC	CACCGCCGTA
9051	ATGCAAAGGA	TAGCACTCCC	ACTCTACTAC	TGGGTATCAT	ATGCTGACTG
	TACGTTTCCT	ATCGTGAGGG	${\tt TGAGATGATG}$	ACCCATAGTA	TACGACTGAC
9101	TATATGCATG	AGGATAGCAT	ATGCTACCCG	GATACAGATT	AGGATAGCAT
	ATATACGTAC	TCCTATCGTA	${\tt TACGATGGGC}$	CTATGTCTAA	TCCTATCGTA
9151	ATACTACCCA	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT
	TATGATGGGT	CTATATCTAA	$\mathtt{TCCTATCGTA}$	TACGATGGGT	CTATATCTAA
9201	AGGATAGCCT	ATGCTACCCA	GATATAAATT	AGGATAGCAT	ATACTACCCA
	TCCTATCGGA	TACGATGGGT	${\tt CTATATTTAA}$	TCCTATCGTA	TATGATGGGT
9251	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT	AGGATAGCCT
	CTATATCTAA	TCCTATCGTA	${\tt TACGATGGGT}$	CTATATCTAA	TCCTATCGGA
9301	ATGCTACCCA	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT
	TACGATGGGT	CTATATCTAA	${\tt TCCTATCGTA}$	${\tt TACGATGGGT}$	CTATATCTAA
9351		${\tt ATGCTATCCA}$			
	TCCTATCGTA	TACGATAGGT	${\tt CTATAAACCC}$	ATCATATACG	ATGGGTCTAT
9401		TAGCATATAC			
	ATTTAATCCT	ATCGTATATG	ATGGGATTAG	AGATAATCCT	ATCGTATACG
9451		CAGATTAGGA			
	ATGGGCCTAT	GTCTAATCCT	ATCGTATATG	${\tt ATGGGTCTAT}$	ATCTAATCCT
9501		${\tt TACCCAGATA}$			
	ATCGTATACG	ATGGGTCTAT	ATCTAATCCT	ATCGGATACG	ATGGGTCTAT
9551	TAAATTAGGA	TAGCATATAC	TACCCAGATA	TAGATTAGGA	TAGCATATGC
	ATTTAATCCT	ATCGTATATG	ATGGGTCTAT	ATCTAATCCT	ATCGTATACG
9601		${\tt TAGATTAGGA}$			
	ATGGGTCTAT	ATCTAATCCT	ATCGGATACG	${\tt ATGGGTCTAT}$	ATCTAATCCT

9651	TAGCATATGC	ТАТССАСАТА	ጥጥጥርርር ርጥ አርጥ	ATATGCTACC	CAMCCCAACA
				TATACGATGG	
9701				AATATGAGGA	
				TTATACTCCT	
9751	TGTGCTTGGC	GCTCAGGCGC	AAGTGTGTGT	AATTTGTCCT	CCAGATCGCA
				TTAAACAGGA	
9801				CTACTTATGC	
				GATGAATACG	
9851				${\tt TGGTTTGACC}$	
0001				ACCAAACTGG	
9901				CCTTATTTTA	
9951				GGAATAAAAT	
9931				GCCCCCACTC CGGGGGTGAG	
10001				TGGGCCCCAT	
				ACCCGGGGTA	
10051				AACCAGTGGA	
				TTGGTCACCT	
10101				AAATAGAGTG	
				TTTATCTCAC	
10151				CATCTTAATA	
				${\tt GTAGAATTAT}$	
10201				AGCCATAAAT	
10051				TCGGTATTTA	
10251				CCCCATGGAT	
10301				GGGGTACCTA	
10301	TTTCTATAG	TCTTACAAAG	TAACCATCTC	TAGTATTTAT ATCATAAATA	TGCCCAAGGG
10351				CAATGCCACC	
				GTTACGGTGG	
10401				TGAAACCTTG	
				ACTTTGGAAC	
10451	CCTCACATAC	ACCTTACTGT	TCACAACTCA	GCAGTTATTC	TATTAGCTAA
				CGTCAATAAG	
10501				TCAGGAGAGT	
40==4				AGTCCTCTCA	
10551				CTAAAATGGT	
10601				GATTTTACCA	
10001	GCACCTTAGG	ACTGGGGTAC	TAAATAAAAC	CGTGACAGCT GCACTGTCGA	CATGGGGTGG
10651				CTAACCCTAA	
-0031				GATTGGGATT	
10701				GAATTAGGGT	
				CTTAATCCCA	
10751				TACCCGTTTA	
				ATGGGCAAAT	

10801			TGCTAATGCC		
40054			ACGATTACGG		
10851			TGATTGACGT		
			ACTAACTGCA		
10901			ACATGTCCCC		
	AAGGACCCGG	GGACCCTCCA	TGTACAGGGG	GTCGTAACCA	CATTCTCGAA
10951			AGGCAATGTT		
	GTCGGTTCTC	AATGTGTATT	TCCGTTACAA	CACAACGTCA	GGTGTCTGAC
11001			AAGCCACTCA		
	GTTTCAGACG	AGGTCCTACT	TTCGGTGAGT	CACAACCGTT	TACACGTGTA
11051	CCATTTATAA	GGATGTCAAC	TACAGTCAGA	GAACCCCTTT	GTGTTTGGTC
	GGTAAATATT	CCTACAGTTG	ATGTCAGTCT	CTTGGGGAAA	CACAAACCAG
11101	CCCCCCGTG	TCACATGTGG	AACAGGGCCC	AGTTGGCAAG	TTGTACCAAC
	GGGGGGCAC	AGTGTACACC	TTGTCCCGGG	TCAACCGTTC	AACATGGTTG
11151	CAACTGAAGG	GATTACATGC	ACTGCCCCGC	GAAGAAGGGG	CAGAGATGCC
	GTTGACTTCC	CTAATGTACG	TGACGGGGCG	CTTCTTCCCC	GTCTCTACGG
11201	GTAGTCAGGT	TTAGTTCGTC	CGGCGGCGGG	GCTCTAGAGT	CGACCGGTCA
	CATCAGTCCA	AATCAAGCAG	GCCGCCGCCC	CGAGATCTCA	GCTGGCCAGT
11251	TGGCTGCGCC	CCGACACCCG	CCAACACCCG	CTGACGCGCC	CTGACGGGCT
	ACCGACGCGG	GGCTGTGGGC	GGTTGTGGGC	GACTGCGCGG	GACTGCCCGA
11301	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCG	TCTCCGGGAG
	ACAGACGAGG	GCCGTAGGCG	AATGTCTGTT	CGACACTGGC	AGAGGCCCTC
11351	CTGCATGTGT	CAGAGGTTTT	CACCGTCATC	ACCGAAACGC	GCGAGGCAGC
			,GTGGCAGTAG		
11401	CGGATCATAA	TCAGCCATAC	CACATTTGTA	GAGGTTTTAC	TTGCTTTAAA
	GCCTAGTATT	AGTCGGTATG	GTGTAAACAT	CTCCAAAATG	AACGAAATTT
11451	AAACCTCCCC	ACCTCCCCCT	GAACCTGAAA	CATAAAATGA	ATGCAATTGT
			CTTGGACTTT		
11501			CAGCTTATAA		
			GTCGAATATT		
11551			AAAGCATTTT		
			TTTCGTAAAA		
11601			TGTATCTTAT		
			ACATAGAATA		
11651			GGGAGATCCG		
			CCCTCTAGGC		
11701			AGAGCCGGCA		
			TCTCGGCCGT		
11751			AGGGACGTAG		
			TCCCTGCATC		
11801			CGAGCAGCCA		
, 11001			GCTCGTCGGT		
11851			TCAGTGCCCA		
			AGTCACGGGT		
11901			GATGAGTTCC		
11201			CTACTCAAGG		
	5155555511	202100000	CILICICHAGG	COCCACCGII	ALCCCICCC

11951			GGAGCTGACA		
	CTTTCGCTTT	CAGGGCCTTT	CCTCGACTGT	CCACCACCGT	TACGGGGTTG
12001	CAGTGGGGGT	TGCGTCAGCA	AACACAGTGC	ACACCACGCC	ACGTTGCCTG
	GTCACCCCCA	ACGCAGTCGT	TTGTGTCACG	TGTGGTGCGG	TGCAACGGAC
12051	ACAACGGGCC	ACAACTCCTC	ATAAAGAGAC	AGCAACCAGG	ATTTATACAA
	TGTTGCCCGG	TGTTGAGGAG	${\tt TATTTCTCTG}$	TCGTTGGTCC	TAAATATGTT
12101	GGAGGAGAAA	ATGAAAGCCA	TACGGGAAGC	AATAGCATGA	TACAAAGGCA
	CCTCCTCTTT	TACTTTCGGT	${\tt ATGCCCTTCG}$	${\tt TTATCGTACT}$	ATGTTTCCGT
12151	TTAAAGCAGC	${\tt GTATCCACAT}$	AGCGTAAAAG	GAGCAACATA	GTTAAGAATA
	AATTTCGTCG	CATAGGTGTA	TCGCATTTTC	CTCGTTGTAT	CAATTCTTAT
12201	CCAGTCAATC	${\tt TTTCACAAAT}$	TTTGTAATCC	AGAGGTTGAT	TC
	GGTCAGTTAG	AAAGTGTTTA	AAACATTAGG	TCTCCAACTA	AG



1	TCGAGCGGCC GCTTTAAACT CAATGGTGAT GGTGATGATG ACCGGTACGC
	AGCTCGCCGG CGAAATTTGA GTTACCACTA CCACTACTAC TGGCCATGCG
-3	HHHHHGTRT
51	GTAGAATCGA GACCGAGGAG AGGGTTAGGG ATAGGCTTAC CGAATTCGAG
	CATCTTAGCT CTGGCTCCTC TCCCAATCCC TATCCGAATG GCTTAAGCTC
-3	TSD L G L L P N P I P K G F E L
101	CTGGGTCACC ATGCCGCTGG CTTCGGAGTG AGTCTTTATG GCCTGGAAGA
	GACCCAGTGG TACGGCGACC GAAGCCTCAC TCAGAAATAC CGGACCTTCT
-3	Q T V M G S A E S H T K I A Q F I
151	TCCACTCCCG GAAGTCACTG ACTTTGGTGT AGACGCCTGG CTTCTGGGCC
	AGGTGAGGGC CTTCAGTGAC TGAAACCACA TCTGCGGACC GAAGACCCGG
-3	IWERFDS V KTY V G P K Q A L
201	AGGGCACAGC CAGTGCCCCA ACTCACAATG CCACACAGCC GCCAACGTGG
	TCCCGTGTCG GTCACGGGGT TGAGTGTTAC GGTGTGTCGG CGGTTGCACC
-3	·LACGTGWSVIGCLRWRP
251	CGTCCGAGAG ATGCTGTCCT CACACACAAA GGGACCACCG CTGTCGCCCT
	GCAGGCTCTC TACGACAGGA GTGTGTGTTT CCCTGGTGGC GACAGCGGGA
-3	TRSISDECVFPGGSDGQ
301	GGCAGGCATC AATGCCACCC TCGGGGTAGC CAGCACAGAA CATCTTGGGC
	CCGTCCGTAG TTACGGTGGG AGCCCCATCG GTCGTGTCTT GTAGAACCCG
-3	·QCADIGGEPYGACFMKPK
351	TTGATCTGGT TTCCATAGAA ATCAGCGCCA TTGCAGACAT CATTGCTGAT
	AACTAGACCA AAGGTATCTT TAGTCGCGGT AACGTCTGTA GTAACGACTA
	THICOTOTICAL THICOTOTICAL TRANSPORTER
-3	
-3 401	
	·KIQNGYFDAGNCVDNSI
	·K Q N G Y F D A G N C V D N S TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT
401	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA
401	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q
401	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC
401 -3 451	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG
401 -3 451	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q
401 -3 451	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG
401 -3 451 -3 501	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC
-3 451 -3 501	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L
-3 451 -3 501	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N
401 -3 451 -3 501 -3 551	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC
401 -3 451 -3 501 -3 551	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N
401 -3 451 -3 501 -3 551	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V A Q V G
401 -3 451 -3 501 -3 551 -3 601	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V A Q V G CCCAGCTGCA GACCGTGGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC
401 -3 451 -3 501 -3 551 -3 601	K I Q N G Y F D A G N C V D N S I TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V A Q V G
401 -3 451 -3 501 -3 551 -3 601	K I Q N G Y F D A G N C V D N S ! TATGGGGACT CGAGCCTCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGTCCCG AAAGGGAAGA TACCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V V A Q V G CCCAGCTGCA GACCGTGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC GGGTCGACGT CTGGCACCC TCTCCGGACC CGGCCACGCCAC
401 -3 451 -3 501 -3 551 -3 601 -3 651	K I Q N G Y F D A G N C V D N S ! TATGGGGACT CGAGCCTCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGGTCCCG AAAGGGAAGA TACCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V V A Q V G CCCAGCTGCA GACCGTGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC GGGTCGACGT CTGGCACCC TCTCCGGACC CGGCACAGCACA
401 -3 451 -3 501 -3 651 -3	K I Q N G Y F D A G N C V D N S ! TATGGGGACT CGAGCCTCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGTCCCG AAAGGGAAGA TACCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V V A Q V G CCCAGCTGCA GACCGTGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC GGGTCGACGT CTGGCACCC TCTCCGGACC CGGCCACGCCAC
401 -3 451 -3 501 -3 651 -3	K I Q N G Y F D A G N C V D N S ! TATGGGGACT CGAGCCTCT GGAGTACCCC GGCCTGTTGG CCATAGTACT ATACCCCTGA GCTCGGAGA CCTCATGGGG CCGGACAACC GGTATCATGA I P V R A E Q L V G A Q Q G Y Y Q O GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG Q I N G W G I V I C I K G D V L A Q TGGCCGGCAG CTGGGAGGA CACAGGCTGG ATGTATTCTG TGAGGGGCAG ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCGTC Q G A A P L C V P Q I Y E I L P L GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA P S S L H V L A I D N S N E E S N TGGGGGTCCCG AAAGGGAAGA TACCCCCGT GGTAGACCAC AGCCTGCACC ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG N P D R F P L Y G G H Y V V V A Q V G CCCAGCTGCA GACCGTGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC GGGTCGACGT CTGGCACCC TCTCCGGACC CGGCACAGCACA

751	TCAGCACCCA GT				
_	AGTCGTGGGT CA				·
-3	_		L S G	G C L	H A G D
801	TCATAGCGAA GC				
_	AGTATCGCTT CO				ACCACAGGGC
-3	·DYRL	s v Q		RGLS	
851	GCCTCCCACG AT				
	CGGAGGGTGC TA	AGAACAGCA	GCAGCAGGTG	CCCGTCGAAG	GACGCCGGTG
-3	GGVI	K D D	D D V	PLK	R R G C
901	AGTCTTGGTC CC				
	TCAGAACCAG GC	CCTCGCAGT	GGTCACCTTG	GACCTTGGGT	CTCGTCGTCA
_			G T S G		L L L V
951	ACCCATAGCA GO				
	TGGGTATCGT CO	CTCACACAG	ACAGAGGTAC	CACCGCTAGA	CCATGGGTCG
-3	·VWLL	L T D	T E M		
1001	TTCTAGAGAT CT				
	AAGATCTCTA GA				
1051	CACCGTACAC GO				
	GTGGCATGTG CO	GGATGGCGG	GTAAACGCAG	TTGCCCCGCC	CCAATAATGC
1101	ACATTTTGGA A				
	TGTAAAACCT TT	rcagggcaa	CTAAAACCAC	GGTTTTGTTT	GAGGGTAACT
1151	CGTCAATGGG GT				
	GCAGTTACCC CA	ACCTCTGAA	CCTTTAGGGG	CACTCAGTTT	GGCGATAGGT
1201	CGCCCATTGG TO				
	GCGGGTAACC AC	CATGACGGT	TTTGGCGTAG	TGGTACCATT	ATCGCTACTG
1251	TAATACGTAG AT				
	ATTATGCATC TA	ACATGACGG	TTCATCCTTT	CAGGGCATTC	CAGTACATGA
1301	GGGCATAATG CO				
	CCCGTATTAC GO	STCCGCCCG	GTAAATGGCA	GTAACTGCAG	TTATCCCCCG
1351	GGACTTGGCA TA				
	CCTGAACCGT AT				
1401	TAAATACTCC AC				
	ATTTATGAGG TO	GGTAACTG	CAGTTACCTT	TCAGGGATAA	CCGCAATGAT
1451	TGGGAACATA CO				
	ACCCTTGTAT GO				
1501	CAGCCAGGCG GG				
	GTCGGTCCGC CC				
1551	TGGGCTATGA AC				
	ACCCGATACT TO	GATTACTGG	GGCATTAACT	AATGATAATT	ATTGATCAGT
1601	ATAATCAATG TO				
	TATTAGTTAC A				
1651	TACATATTAT GA				
	ATGTATAATA C	TATATCTAT	GTTGCATACG	TTACCGGTTA	TCGGTTATAA
1701	GATTTATGCT A				
	CTAAATACGA T	ATATTGGTT	ACTGATTATA	CCGATTAACG	GTTATAACTA

1751			ACCTACCAGT		
			TGGATGGTCA		
1801			GATGATAAGC		
			CTACTATTCG		
1851			AAATCCGCGC		
			TTTAGGCGCG		
1901			GCCCGGTGTT		
			CGGGCCACAA		
1951			AAAAACCATG		
			TTTTTGGTAC		
2001			AACGCCCAAA		
			TTGCGGGTTT		
2051			ACCCCGTCCC		
04.04			TGGGGCAGGG		
2101			CGACGTTGGC		
0151			GCTGCAACCG		
2151			GGGGAAAAGG		
2201			CCCCTTTTCC		
2201			GGTATCGACA		
2251			CCATAGCTGT		
2251			ACGACCCAAC TGCTGGGTTG		
2301					
2301			GCGGGTTCCT CGCCCAAGGA	_	
2351					
Z331			ATCTCCCCTA TAGAGGGGAT		
2401			CTATCGGCGA		
2401			GATAGCCGCT		
2451			GCGGGCGATT		
2431			CGCCCGCTAA		
2501			CGTCGCATCG		
2301			GCAGCGTAGC		
2551			AAGCTCTGAT		
2001			TTCGAGACTA		
2601			CCGCGGCGAT		
	~				GGCCTACGGA
2651			GCTGCTCCAT		
					GTGCCGGAGG
2701					CATCGCCTCG
			AGCATAACCC		
2751	CTCCAGTCAA	TGACCGCTGT	TATGCGGCCA	TTGTCCGTCA	GGACATTGTT
					CCTGTAACAA
2801					CAGTCCTCGG
					GTCAGGAGCC
2851	CCCAAAGCAT	CAGCTCATCG	AGAGCCTGCG	CGACGGACGC	ACTGACGGTG
					TGACTGCCAC

FLGURE 11-3

2901		CAGTTTGCCA			
		GTCAAACGGT			
2951		CGCCATGTAG			
	ATACTTTAGT	GCGGTACATC	ACATAACTGG	CTAAGGAACG	CCAGGCTTAC
3001	GGCCGAACCC	GCTCGTCTGG	CTAAGATCGG	CCGCAGCGAT	CGCATCCATG
	CCGGCTTGGG	CGAGCAGACC	GATTCTAGCC	GGCGTCGCTA	GCGTAGGTAC
3051	GCCTCCGCGA	CCGGCTGCAG	AACAGCGGGC	AGTTCGGTTT	CAGGCAGGTC
		GGCCGACGTC			
3101		ACACCCTGTG			
		TGTGGGACAC			
3151		CCCAATGTCA			
		GGGTTACAGT			
3201		GATAAACATA			
0201		CTATTTGTAT			
3251		AGGACATATC			
3231		TCCTGTATAG			
3301		GCCCTCCGAG			
5501		CGGGAGGCTC			
3351					
2221		GAAACTTCTC CTTTGAAGAG			
3401					
34UI		TGCCCGGGAT			
2451		ACGGGCCCTA			
3451		GGTCGCTCGG			
2504		CCAGCGAGCC			
3501		CCTGGGACCG			
		GGACCCTGGC			
3551		ACAAGACGCT			
		TGTTCTGCGA			
3601		TATATTTCTT			
	CTGTACGTTT	ATATAAAGAA	GGCCCCTGTG	GCGGTCGTTT	GCGCTCGTTG
3651		GATGAAGCAG			
		CTACTTCGTC			
3701	TTGCTGGCGT	TCGCGACGCG	AGGCTGGATG	GCCTTCCCCA	TTATGATTCT
	AACGACCGCA	AGCGCTGCGC	TCCGACCTAC	CGGAAGGGGT	AATACTAAGA
3751	TCTCGCTTCC	GGCGGCATCG	GGATGCCCGC	GTTGCAGGCC	ATGCTGTCCA
	AGAGCGAAGG	CCGCCGTAGC	CCTACGGGCG	CAACGTCCGG	TACGACAGGT
3801		TGACGACCAT			
	CCGTCCATCT	ACTGCTGGTA	GTCCCTGTCG	AAGTTCCTAG	CGAGCGCCGA
3851	CTTACCAGCC	TAACTTCGAT	CACTGGACCG	CTGATCGTCA	CGGCGATTTA
	GAATGGTCGG	ATTGAAGCTA	GTGACCTGGC	GACTAGCAGT	GCCGCTAAAT
3901	TGCCGCCTCG	GCGAGCACAT	GGAACGGGTT	GGCATGGATT	GTAGGCGCCG
		CGCTCGTGTA			
3951	CCCTATACCT	TGTCTGCCTC	CCCGCGTTGC	GTCGCGGTGC	ATGGAGCCGG
		ACAGACGGAG			
4001		CCTGAATGGA			
					GCCTAAGTGG

4051		TTGGAGCCAA AACCTCGGTT			
4101		TGGCAGAACA ACCGTCTTGT			
4151		CAGCAAAAGG			
4131		GTCGTTTTCC			
4201	CGTTTTTCCA	TAGGCTCCGC	CCCCTGACG	AGCATCACAA	AAATCGACGC
		ATCCGAGGCG			
4251	TCAAGTCAGA	GGTGGCGAAA	CCCGACAGGA	CTATAAAGAT	ACCAGGCGTT
	${\tt AGTTCAGTCT}$	${\tt CCACCGCTTT}$	GGGCTGTCCT	GATATTTCTA	TGGTCCGCAA
4301	TCCCCCTGGA	AGCTCCCTCG	TGCGCTCTCC	TGTTCCGACC	CTGCCGCTTA
		TCGAGGGAGC			
4351	CCGGATACCT	GTCCGCCTTT	CTCCCTTCGG	GAAGCGTGGC	GCTTTCTCAT
		CAGGCGGAAA			
4401		GTAGGTATCT			
		CATCCATAGA			
4451		CACGAACCCC			
		GTGCTTGGGG			
4501		TCTTGAGTCC			
1301		AGAACTCAGG			
4551		CTGGTAACAG			•
1331		GACCATTGTC			
4601		TTGAAGTGGT			
.1001		AACTTCACCA			
4651		CTGCGCTCTG			
4031		GACGCGAGAC			
4701		GATCCGGCAA			
4/01		CTAGGCCGTT			
4751					
4/31		CAGCAGATTA GTCGTCTAAT			
4001					
4801		TTCTACGGGG AAGATGCCCC			
4051					
4851		TGGTCATGAG			
4004		ACCAGTACTC			
4901		AAATGAAGTT			
		TTTACTTCAA			
4951		CAGTTACCAA			
		GTCAATGGTT			
5001		TTCGTTCATC			
		AAGCAAGTAG			
5051		CGGGAGGGCT			
		GCCCTCCCGA			
5101					AAACCAGCCA
		TGCGAGTGGC			
5151		CCGAGCGCAG			
	CGGCCTTCCC	GGCTCGCGTC	TTCACCAGGA	CGTTGAAATA	GGCGGAGGTA

5201		AATTGTTGCC			
F0F4		TTAACAACGG			
5251		CAACGTTGTT			
		GTTGCAACAA			
5301		GTATGGCTTC			
	AGCAGCAAAC	CATACCGAAG	TAAGTCGAGG	CCAAGGGTTG	CTAGTTCCGC
5351		TCCCCCATGT			
		AGGGGGTACA			
5401		TGTCAGAAGT			
	GAGGCTAGCA	ACAGTCTTCA	TTCAACCGGC	GTCACAATAG	TGAGTACCAA
5451	ATGGCAGCAC	TGCATAATTC	TCTTACTGTC	ATGCCATCCG	TAAGATGCTT
	TACCGTCGTG	ACGTATTAAG	AGAATGACAG	TACGGTAGGC	ATTCTACGAA
5501	TTCTGTGACT	GGTGAGTACT	CAACCAAGTC	ATTCTGAGAA	TAGTGTATGC
		CCACTCATGA			
5551	GGCGACCGAG	TTGCTCTTGC	CCGGCGTCAA	CACGGGATAA	TACCGCGCCA
		AACGAGAACG			
5601	CATAGCAGAA	CTTTAAAAGT	GCTCATCATT	GGAAAACGTT	CTTCGGGGCG
		GAAATTTTCA			
5651	AAAACTCTCA	AGGATCTTAC	CGCTGTTGAG	ATCCAGTTCG	ATGTAACCCA
		TCCTAGAATG			
5701	CTCGTGCACC	CAACTGATCT	TCAGCATCTT	TTACTTTCAC	CAGCGTTTCT
		GTTGACTAGA			
5751		AAACAGGAAG			
		TTTGTCCTTC			
5801	GACACGGAAA	TGTTGAATAC	TCATACTCTT	CCTTTTTCAA	TATTATTGAA
		ACAACTTATG			
5851	GCATTTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT	TGAATGTATT
		CCCAATAACA			
5901		AACAAATAGG			
		TTGTTTATCC			
5951		TAAGAAACCA			
		ATTCTTTGGT			
6001		GAGGCCCTTT			
		CTCCGGGAAA			
6051		AAGCTGATCC			
		TTCGACTAGG			
6101		CATCTCTGTC			
		GTAGAGACAG			
6151		CCATCCCTAC			
		GGTAGGGATG			
6201		TGAGGCTCAG			
		ACTCCGAGTC			
6251		TGCGAGTAAT			
		ACGCTCATTA			
6301		TCAGACCTGG			
		AGTCTGGACC			
			0110110ITC1	ALCOCIGGIA	CITCCCCIAC

6351		GGGGGCAGGA	
C 4 0 1		CCCCCGTCCT	
6401		ATGTCTATTG	
		TACAGATAAC	
6451		ACAGGACCTG	
		TGTCCTGGAC	
6501		AGGCTCCGGC	
		TCCGAGGCCG	
6551		GAGGACGGGG	
		CTCCTGCCCC	
6601		${\tt GGCGGCTCAG}$	
		CCGCCGAGTC	
6651		AAAACGTCCA	
		TTTTGCAGGT	
6701		CAGGAGCAGG	
		GTCCTCGTCC	
6751		GGGGCAGGAG	
		CCCCGTCCTC	
6801		AGGAGCAGGA	
6051		TCCTCGTCCT	
6851		GGGCAGGAGC	
6901		CCCGTCCTCG	
0901		GGAGCAGGAG CCTCGTCCTC	
6951			
0731		GGCAGGAGCA CCGTCCTCGT	
7001			
,001		GAGGGGCAGG CTCCCCGTCC	
7051		GGAGGGGCAG	
, 031		CCTCCCCGTC	
7101		AGGAGGGGCA	
		TCCTCCCCGT	
7151		GAGCAGGAGG	
		CTCGTCCTCC	
7201		GCAGGAGGG	
		CGTCCTCCCC	
7251		GGCAGGAGGG	
		CCGTCCTCCC	
7301		GGGCAGGAGG	
		CCCGTCCTCC	
7351		GCAGGAGGG	
		CGTCCTCCC	
7401		AGGAGGTGGA	
		TCCTCCACCT	
7451		GTAGTGGAGG	
		CATCACCTCC	

FIGURE 11-7

7501	GAGGCCGCCG CTCCGGCGGC	GGGTAGAGGA CCCATCTCCT	CGTGAAAGAG GCACTTTCTC	CCAGGGGGGG	AAGTCGTGAA
7551					
7331	TCTCGGTCCC	CCTCTCCAGC	TGGACGTGGA ACCTGCACCT	GAAAAGAGGC CTTTTCTCCG	CCAGGAGTCC GGTCCTCAGG
7601	CAGTAGTCAG	TCATCATCAT	CCGGGTCTCC	ACCGCGCAGG	CCCCCTCCAG
	GTCATCAGTC	AGTAGTAGTA	GGCCCAGAGG	TGGCGCGTCC	GGGGGAGGTC
7651			CCTGTAGGGG		
	CATCTTCCGG	TAAAAAGGTG	GGACATCCCC	TTCGGCTAAT	AAAACTTATG
7701			TGGTGAGCCT		
	GTGGTTCTTC	CACCGGGTCT	ACCACTCGGA	CTGCACGGGG	GCCCTCGCTA
7751	AGAGCAGGGC	CCCGCAGATG	ACCCAGGAGA	AGGCCCAAGC	ACTGGACCCC
	TCTCGTCCCG	GGGCGTCTAC	TGGGTCCTCT	TCCGGGTTCG	TGACCTGGGG
7801			AGGCGCAAAA		
	CCCCAGTCCC	ACTACCTCCG	TCCGCGTTTT	TTCCTCCCAC	CAAACCTTTC
7851			CAACCCGAAA		
	GTAGCACCAG	TTCCTCCAAG	GTTGGGCTTT	AAACTCTTGT	AACCTCTTCC
7901			GGAGTCACGT		
	AAATTCTCGA	GAGGACCGAT	CCTCAGTGCA	TCTTTCCTCA	TCCCTCCTTCC
7951			TTCGTATATG		
	CTTGAACCCA	GCGGCCACAC	AAGCATATAC	GAGGTAGTAA	GACCTCCCTT
8001					
0001	ATCTTCCATT	CCCCTCCTTTC	TGCCCTTGCT	ATTCCACAAT	GTCGTCTTAC
8051			ACGGGAACGA		
903T	TCCTA A CTCA	CGTCTCCCCT	TTGGAATGGC	CCCTGGACCC	GGCCCACAAC
0101			AACCTTACCG		
8101	CTGGCCCGCT	AAGGGAGTCC	ATTGTCTGTT	ATTTCATGGT	CTTTTTACAA
			TAACAGACAA		
8151	ACTCATATAT	TTGCTGAGGT	${\tt TTTGAAGGAT}$	GCGATTAAGG	ACCTTGTTAT
			AAACTTCCTA		
8201	GACAAAGCCC	GCTCCTACCT	GCAATATCAG	GGTGACTGTG	TGCAGCTTTG
	CTGTTTCGGG	CGAGGATGGA	${\tt CGTTATAGTC}$	CCACTGACAC	ACGTCGAAAC
8251			CCCTGGTTTC		
	TGCTACCTCA	TCTAAACGGA	GGGACCAAAG	GTGGATACCA	CCTTCCCCGA
8301	GCCGCGGAGG	GTGATGACGG	AGATGACGGA	GATGAAGGAG	GTGATGGAGA
	CGGCGCCTCC	CACTACTGCC	TCTACTGCCT	CTACTTCCTC	CACTACCTCT
8351	TGAGGGTGAG	GAAGGCAGG	AGTGATGTAA	CTTGTTAGGA	GACGCCCTCA
	ACTCCCACTC	CTTCCCGTCC	TCACTACATT	GAACAATCCT	CTGCGGGAGT
8401			TTCCCCCGCA		
	TAGCATAATT	TTCGGCACAT	AAGGGGGCGT	GATTTCTTAT	TTAGGGGTCA
8451			GTGTATTTCT		
	TCTGTAGTAC	GCACGACAAC	CACATAAAGA	CCGGTAGACA	GAACAGTGGT
8501			GGCAATTGGG		
_	AAAAGCAGGA	GGGTTGTACC	CCGTTAACCC	CTATACCCATG	AACACTCACGTC
8551			CCTTCTCGCG		
	TGAGTCGAGG	CGCGAGTTGT	GGAAGAGCGC	A A COMMUNICATION AND COMMUNIC	TTAGCGACAT
8601					
J U U L	AATGGACCAC	TCCTTACTC	CATGCGACGG	CTTTTAGCCTG	GCCTCCTTAA
	OACCAC	TCGITAGICT	GTACGCTGCC	GAAATCGGAC	CGGAGGAATT

8651			AACCAGCATG		
0701			TTGGTCGTAC		
8701			AGGTGGCGGC		
			TCCACCGCCG		
8751			ATATGCTGAC		
			TATACGACTG		
8801			TTAGGATAGC		
	TATACGATGG	GCCTATGTCT	AATCCTATCG	TATATGATGG	GTCTATATCT
8851	TTAGGATAGC	ATATGCTACC	CAGATATAGA	TTAGGATAGC	CTATGCTACC
	AATCCTATCG	TATACGATGG	GTCTATATCT	AATCCTATCG	GATACGATGG
8901	CAGATATAAA	TTAGGATAGC	ATATACTACC	CAGATATAGA	TTAGGATAGC
	GTCTATATTT	AATCCTATCG	TATATGATGG	GTCTATATCT	AATCCTATCG
8951	ATATGCTACC	CAGATATAGA	TTAGGATAGC	CTATGCTACC	CAGATATAGA
			AATCCTATCG		
9001	TTAGGATAGC	ATATGCTACC	CAGATATAGA	TTAGGATAGC	ATATGCTATC
			GTCTATATCT		
9051			GCTACCCAGA		
			CGATGGGTCT		
9101			GATAGCATAT		
			CTATCGTATA		
9151			TATAGATTAG		
			ATATCTAATC		
9201			GCTACCCAGA		
			CGATGGGTCT		
9251			GATAGCATAT		
3232			CTATCGTATA		
9301			TATAGATTAG		
J J U I			ATATCTAATC		
9351					
9331			CCCATGGCAA GGGTACCGTT		
9401					
9401			GACCAACAAC		
0451			CTGGTTGTTG		
9451			CTCCAGATCG		
0501			GAGGTCTAGC		
9501			GCAGGTATTC		
			CGTCCATAAG		
9551			CCGCAGTGGT		
			GGCGTCACCA		
9601			TACAGTCCAA		
			ATGTCAGGTT		
9651			TCCACAATTT		
			AGGTGTTAAA		
9701			ATTGGCGTGG		
			TAACCGCACC		
9751			GAGTCCGCTG		
	CCACAATCTC	TGTTGGTCAC	CTCAGGCGAC	GACAGCCGCA	GGTGAGAGAA

pCEP4W/hep36

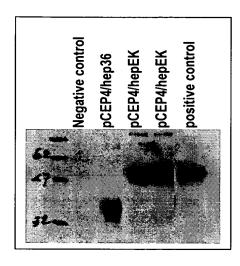
9801		ACAAATAGAG TGTTTATCTC			
9851	CTGCCTGGGA	CACATCTTAA GTGTAGAATT	TAACCCCAGT	ATCATATTGC	ACTAGGATTA
9901	TGTGTTGCCC	ATAGCCATAA	ATTCGTGTGA	GATGGACATC	CAGTCTTTAC
9951	GGCTTGTCCC	TATCGGTATT CACCCCATGG GTGGGGTACC	ATTTCTATTG	TTAAAGATAT	TCAGAATGTT
10001	TCATTCCTAC	ACTAGTATTT TGATCATAAA	ATTGCCCAAG	GGGTTTGTGA	GGGTTATATT
10051	GGTGTCATAG	CACAATGCCA GTGTTACGGT	CCACTGAACC	CCCCGTCCAA	ATTTTATTCT
10101	GGGGGCGTCA	CCTGAAACCT GGACTTTGGA	TGTTTTCGAG	CACCTCACAT	ACACCTTACT
10151	GTTCACAACT	CAGCAGTTAT GTCGTCAATA	TCTATTAGCT	AAACGAAGGA	GAATGAAGAA
10201	GCAGGCGAAG	ATTCAGGAGA TAAGTCCTCT	GTTCACTGCC	CGCTCCTTGA	TCTTCAGCCA
10251	CTGCCCTTGT	GACTAAAATG CTGATTTTAC	GTTCACTACC	CTCGTGGAAT	CCTGACCCCA
10301	TGTAAATAAA	ACCGTGACAG TGGCACTGTC	CTCATGGGGT	GGGAGATATC	GCTGTTCCTT
10351	AGGACCCTTT	TACTAACCCT ATGATTGGGA	AATTCGATAG	CATATGCTTC	CCGTTGGGTA
10401	ACATATGCTA	TTGAATTAGG AACTTAATCC	GTTAGTCTGG	ATAGTATATA	CTACTACCCG
10451	GGAAGCATAT	GCTACCCGTT CGATGGGCAA	TAGGGTTAAC	AAGGGGGCCT	TATAAACACT
10501	ATTGCTAATG	CCCTCTTGAG GGGAGAACTC	GGTCCGCTTA	TCGGTAGCTA	CACAGGCCCC
10551	TCTGATTGAC	GTTGGTGTAG CAACCACATC	CCTCCCGTAG	TCTTCCTGGG	CCCCTGGGAG
10601		CCCAGCATTG GGGTCGTAAC			
10651		TTGTGTTGCA AACACAACGT			
10701		CAGTGTTGGC GTCACAACCG			
10751		GAGAACCCCT CTCTTGGGGA			
10801		CCAGTTGGCA GGTCAACCGT			
10851		GCGAAGAAGG CGCTTCTTCC			
10901		GGGCTCTAGA CCCGAGATCT			

FIGURE 11-10

pCEP4W/hep36

40054					
10951	CGCCAACACC	CGCTGACGCG	CCCTGACGGG	CTTGTCTGCT	CCCGGCATCC
		GCGACTGCGC			
11001	GCTTACAGAC	AAGCTGTGAC	CGTCTCCGGG	AGCTGCATGT	GTCAGAGGTT
		TTCGACACTG			
11051		TCACCGAAAC			
•		AGTGGCTTTG			
11101	ACCACATTTG	TAGAGGTTTT	ACTTGCTTTA	AAAAACCTCC	CCACCTCCCC
		ATCTCCAAAA			
11151		AACATAAAAT			
		TTGTATTTTA			
11201	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA	TAGCATCACA	AATTTCACAA
	ACGTCGAATA	TTACCAATGT	TTATTTCGTT	${\tt ATCGTAGTGT}$	TTAAAGTGTT
11251	ATAAAGCATT	${\tt TTTTTCACTG}$	${\tt CATTCTAGTT}$	GTGGTTTGTC	CAAACTCATC
		AAAAAGTGAC			
11301		${\tt ATCATGTCTG}$			
		TAGTACAGAC			
11351	AAGGGAGATC	${\tt CGACTCGTCT}$	GAGGGCGAAG	GCGAAGACGC	GGAAGAGGCC
		GCTGAGCAGA			
11401	GCAGAGCCGG	CAGCAGGCCG	CGGGAAGGAA	GGTCCGCTGG	ATTGAGGGCC
		GTCGTCCGGC			
11451	GAAGGGACGT	AGCAGAAGGA	CGTCCCGCGC	AGAATCCAGG	TGGCAACACA
		TCGTCTTCCT			
11501	GGCGAGCAGC	CAAGGAAAGG	ACGATGATTT	CCCCGACAAC	ACCACGGAAT
	CCGCTCGTCG	GTTCCTTTCC	TGCTACTAAA	$\tt GGGGCTGTTG$	TGGTGCCTTA
11551	TGTCAGTGCC	CAACAGCCGA	GCCCCTGTCC	AGCAGCGGGC	AAGGCAGGCG
		GTTGTCGGCT			
11601	GCGATGAGTT	CCGCCGTGGC	AATAGGGAGG	GGGAAAGCGA	AAGTCCCGGA
	CGCTACTCAA	GGCGGCACCG	TTATCCCTCC	CCCTTTCGCT	TTCAGGGCCT
11651		CAGGTGGTGG			
	TTCCTCGACT	GTCCACCACC	GTTACGGGGT	TGGTCACCCC	CAACGCAGTC
11701	CAAACACAGT	GCACACCACG	CCACGTTGCC	TGACAACGGG	CCACAACTCC
	GTTTGTGTCA	CGTGTGGTGC	GGTGCAACGG	ACTGTTGCCC	GGTGTTGAGG
11751	TCATAAAGAG	ACAGCAACCA	GGATTTATAC	AAGGAGGAGA	AAATGAAAGC
	AGTATTTCTC	TGTCGTTGGT	CCTAAATATG	TTCCTCCTCT	TTTACTTTCG
11801		GCAATAGCAT			
		CGTTATCGTA			
11851	ATAGCGTAAA	AGGAGCAACA	TAGTTAAGAA	TACCAGTCAA	TCTTTCACAA
	TATCGCATTT	TCCTCGTTGT	ATCAATTCTT	ATGGTCAGTT	AGAAAGTGTT
11901		CCAGAGGTTG			
	TAAAACATTA	GGTCTCCAAC	TAAG		

Figure 12: Western Blot of Hepsin expressed in 293EBNA cells. 4 days after transfection, conditioned medium was harvested. 10 μl of conditioned medium was loaded on a 10% Tris-Glycine gel. Untreated 293EBNA cells served as negative control, 5 ng of purified hepsin ED/EK (expressed from insect cells) served as positive control. After electrophoresis, proteins were transferred onto Nitrocellulose membrane at 100 V for 1h. The membrane was then probed with anti-V5 antibody at 37C° for 1h after blocking with 5% dry milk in TTBS buffer for 1h.



ਜੂ gnedium ₩W Anti-V5 antibody Control cells

planue-purified clone 1
cells + medium plaque-purified clone 2 cells + redium

MW

The purified clone 2 cells + redium

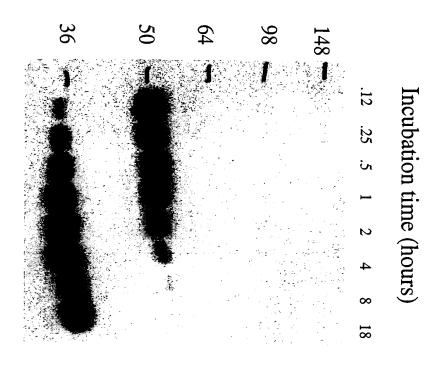
MW

The purified clone 2 cells + redium

The plaque-purified clone 2 cells + redium 48 48 25 3 Anti-His antibody Countrol cells ្សាន្ត្ហីue-purified clone 1 cells + medium plaque-purified clone 2 cells + medium

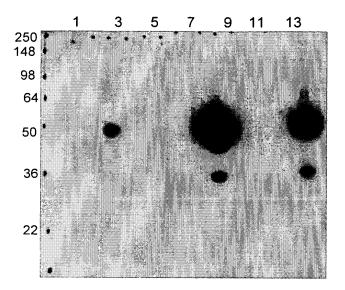
soluble hepsin was present in cultured medium and cell pellets. antibody (left panel) and an anti-His antibody (right panel) showed that recombinant was expressed in baculovirus infected insect cells. Western analysis using an anti-V5 Fig. 13. Western analysis of recombinant soluble hepsin. Recombinant soluble hepsin

Figure 14: Enterokinase (EKMax)processing of Hepsin -ED-EK protein to generate active enzyme



3.1 units EKMax / ml

Figure 15A: Western Slot Blot on the hybridomas 11C1 & 47A5 are WB positive against Hepsin-ED-EK protein.



Blot 1			
slot#	I.D.	CODE	
1	1 2F10		
2	2	9H6	
3	3	11C1	
4	4	16A2	
5	5 27A1		
6	6 30C10		
7	7 30H12		
8	8 35D4		
9	9 47A5		
10	10 80F6		
11	Blank		
12	Blank		
13	Blank		
14	Mouse Poly clonal		

Figure 15B: Western Slot Blot on the hybridomas 31C1 and 38E2 are WB positive against Hepsin-ED-EK protein.

- ·			
Blot 1			
slot#	I.D.	CODE	
1	1	7H3	
2	2	12A2	
3	3	16A3	
4	4	20D1	
5	5	22A3	
6	6	31C1	
7	7	31H2	
8	8	36B2	
9	9	38 E2	
10	10	39D6	
11	11	41F7	
12	12	42 E3	
13	Blank		
14	Mouse Poly clonal		

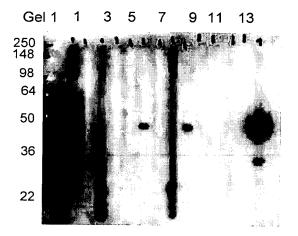
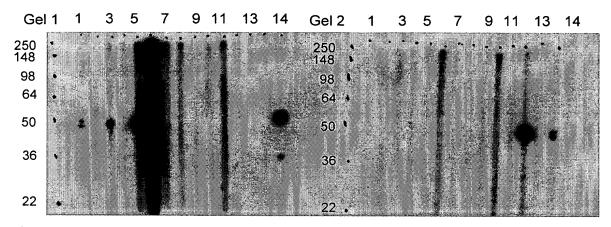


Figure 15C: Western Slot Blot on the hybridomas 37G10, 46D12 & 14C7 are WB positive against Hepsin-ED-EK protein.



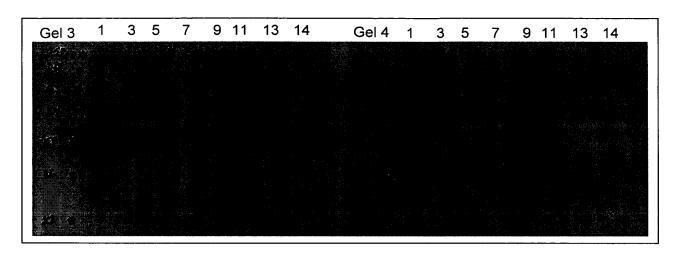
Gel 1

Slot Sample Dilution 1 Rabbit Polyclonal –Cayman Chem 1:500 2 Media neat 3 37G10 " 4 94A7 " 5 46D12 " 6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank 15 Protein - Of mouse 1:5000			
Chem 2	Slot	Sample	Dilution
2 Media neat 3 37G10 " 4 94A7 " 5 46D12 " 6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	1	Rabbit Polyclonal –Cayman	1:500
3 37G10 " 4 94A7 " 5 46D12 " 6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank		Chem	
4 94A7 " 5 46D12 " 6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	2	Media	neat
5 46D12 " 6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	3	37G10	"
6 103E3 " 7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	4	94A7	ti .
7 40F1 " 8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	5	46D12	"
8 103H12 " 9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	6	103E3	"
9 93D1 " 10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	7	40F1	"
10 10C2 " 11 102F2 " 12 83E11 " 13 Blank 14 Blank	8	103H12	"
11 102F2 " 12 83E11 " 13 Blank 14 Blank	9	93D1	"
12 83E11 " 13 Blank 14 Blank	10	10C2	"
13 Blank 14 Blank	11	102F2	tt
14 Blank	12	83E11	tt
	13	Blank	
15 Protein - 07 mouse 1:5000	14	Blank	
	15	Protein - 7 mouse	1:5000

Gel 2

Slot	Comple	Dilution
3101	Sample	Dilution
1	Protein - O ⁷ mouse	1:5000
2	Media	neat
3	27E7	u
4	92A7	"
5	91A4	"
6	99B11	"
7	94C7	"
8	91A1	"
9	14H11	u
10	74C7	"
11	72H6	u
12	14C7	"
13	Blank	
14	Rabbit Polyclonal –Cayman	1:500
	Chem	

Figure 15D: Western Slot Blot on the hybridomas 14C7 & 72H6 are WB positive against Hepsin-ED-EK protein.



Gel 3

Slot	Sample	Dilution
		
1	Protein - 07 mouse	1:5000
2	Media	neat
3	84G6	"
4	84H2	"
5	51F8	"
6	15b11	"
7	90E6	"
8	72H6	"
9	85A4	"
10	87C2	"
11	3G11	"
12	53E11	"
13	91H4	"
14	53C7	"
15	88C7	"

Gel 4

Slot	Sample	Dilution
1	Protein - O mouse	1:5000
2	Media	neat
3	75H3	ti .
4	98B4	66
5	91C9	66
6	53D9	16
7	80G6	66
8	95F3	"
9	14C7	14
10	80H10	11
11	92A9	66
12	81C8	tt
13	96B6	££
14	1812	tt

FIG 16A: Human Prostate Tumor Tissue



Control
Anti-Hepsin mouse
polyclonal preimmun
1/500 (9)

Anti-Hepsin mouse polyclonal immun 1/500 (10)

FIG 16B: Human Prostate Tumor Tissue



Control medium

Anti-Hepsin monoclonal ab (medium)

FIG 16C: Human Prostate Tumor Tissue



Anti-Hepsin monoclonal ab

Figure 17

Human wild-type hepsin amino acid sequence:

maqkeggrtv pccsrpkvaa ltagtllllt aigaaswaiv avllrsdqep lypvqvssad 61 arlmvfdkte gtwrllcssr snarvaglsc eemgflralt hseldvrtag angtsgffcv 121 degrlphtqr llevisvcdc prgrflaaic qdcgrrklpv drivggrdts lgrwpwqvsl 181 rydgahlcgg sllsgdwvlt aahcfpernr vlsrwrvfag avaqasphgl qlgvqavvyh 241 ggylpfrdpn seensndial vhlssplplt eyiqpvclpa agqalvdgki ctvtgwgntq 301 yygqqagvlq earvpiisnd vcngadfygn qikpkmfcag ypeggidacq gdsggpfvce 361 dsisrtprwr lcgivswgtg calaqkpgvy tkvsdfrewi fqaikthsea sgmvtql

the cytoplasmic domain: Met1 to Lys17 the transmembrane domain: Val18 to Leu44

the ectodomain: Arg45 to Leu417

Figure 18

Hep-ED-EK structure (modified soluble hepsin with substitute activation sequence)

```
1 RSDQEPLYPV QVSSADARLM VFDKTEGTWR LLCSSRSNAR VAGLSCEEMG FLRALTHSEL
61 DVRTAGANGT SGFFCVDEGR LPHTQRLLEV ISVCDCPRGR FLAAICQDCG RRKLPVDDDD
121 KIVGGRDTSL GRWPWQVSLR YDGAHLCGGS LLSGDWVLTA AHCFPERNRV LSRWRVFAGA
181 VAQASPHGLQ LGVQAVVYHG GYLPFRDPNS EENSNDIALV HLSSPLPLTE YIQPVCLPAA
241 GQALVDGKIC TVTGWGNTQY YGQQAGVLQE ARVPIISNDV CNGADFYGNQ IKPKMFCAGY
301 PEGGIDACQG DSGGPFVCED SISRTPRWRL CGIVSWGTGC ALAQKPGVYT KVSDFREWIF
361 QAIKTHSEAS GMVTQLEFGK PIPNPLLGLD STRTGHHHHH H*
```

Cytoplasmic domain: absent Transmembrane domain: absent

Modified activation domain:117-121 (underlined)

V5 and 6-His Tag: 377-401

Figure 19



